

OM nucleic - nucleic search, using sw model

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run on:      January 16, 2003, 13:14:12 ; Search time 6222 Seconds
              (without alignments)
              12699.740 Million cell updates/sec

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Title: US-09-817-774-30
Perfect score: 4870

Sequence: 1 aactgtctcctccacaa.....atctaaaaacatttactg 487g

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

```

1: em.estha:*
2: em.estlin:*
3: em.estlin:*
4: em.estmov:*
5: em.estov:*
6: em.estpl:*
7: em.estro:*
8: em.htc:*
9:
10: gb.est:*
11: gb.htc:*
12: gb.est:*
13: gb.est:*
14: gb.est:*
15: em.estlin:*
16: em.estom:*
17: gb.gss:*
18: em.gss.hum:*
19: em.gss.inv:*
20: em.gss.pln:*
21: em.gss.fir:*
22: em.gss.fun:*
23: em.gss.mam:*
24: em.gss.mam:*
25: em.gss.other:*
26: em.gss.pro:*
27: em.gss.roo:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Query No.	Score	Match	length	DB	ID	Description
C 1	608	12.5	625	17	B30087	B30087 T23137FB
C 2	441.2	9.0	447	17	BH170465	BH170465 SALK_0023
C 3	399.8	8.2	631	9	AU238585	AU238585 AU238585
C 4	299.4	6.1	835	17	B18303	B18303 F24B19-SP6
C 5	297	6.1	875	17	BH248541	BH248541 BOGAC47TT
C 6	282.2	5.6	399	10	AV789413	AV789413 AV789413

C	7	280.4	5.7	762	17	BH722372
C	8	258.8	5.3	313	10	BE522479
C	9	252.8	5.3	397	10	AV820534
C	10	252.8	5.1	388	10	AV804475
C	11	247.4	5.2	543	17	CNS00MP7
C	12	231	4.7	421	10	AV810289
C	13	230.2	4.7	410	10	AV817908
C	14	224.8	4.6	457	10	AVS54437
C	15	224	4.6	529	10	AVS53366
C	16	224	4.6	554	10	AV830142
C	17	217.4	4.5	389	10	AV812548
C	18	215.8	4.4	359	10	AV801981
C	19	208.4	4.3	342	10	AVS61130
C	20	192.4	4.3	341	17	BH617242
C	21	186.8	3.8	342	10	AVS26218
C	22	185.4	3.8	460	17	BH170488
C	23	177.8	3.6	724	17	B20222
C	24	177.4	3.6	453	10	AV786514
C	25	167	3.4	740	17	B18763
C	26	157.4	3.2	239	10	BE527244
C	27	145	3.0	358	10	BE530521
C	28	133	2.7	347	10	BE522478
C	29	130.8	2.7	582	14	H76200
C	30	128	2.6	699	9	A1054619
C	31	127.8	2.6	390	14	H76608
C	32	127.4	2.6	583	9	A1993836
C	33	125.8	2.6	497	12	BE601019
C	34	125.8	2.6	508	12	BF053536
C	35	125.8	2.6	517	12	BC096517
C	36	125.8	2.6	549	12	BE097155
C	37	125.8	2.6	599	12	BE597429
C	38	125.8	2.6	630	12	BE593376
C	39	125.8	2.6	660	12	BR053408
C	40	125.8	2.6	696	12	BE592974
C	41	125.8	2.6	700	12	BE597158
C	42	125.8	2.6	722	12	BE599860
C	43	125.8	2.6	742	12	BE599568
C	44	125.8	2.6	749	12	BE596307
C	45	125	2.6	686	12	EG135632

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
B30087	B30087/c	B30087 T25J13TFB TAWU Arabidopsis thaliana genomic clone T25J13, DNA sequence.	B30087	B30087		GSS.	thale cress. Arabidopsis thaliana	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eucosids II; Brassicales; Brassicaceae; Arabidopsids.	Rounsley,S.D., Kelley,J.M., Field,C.E., Craven,M.B., Adams,M.D. and Venter,J.C.	Use of a BAC End Sequence Database To Identify Minimal Overlaps for Arabidopsis Genomic Sequencing	Unpublished (1997)	Other GSSs: T25J13FR
			B30087.1		GI:2516053						Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: rounsley@tigr.org	
												Seq primer: M13-21 Class: BAC ends

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 631)	Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Setou, M., Nakajima, M., Ito, Y., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayasizaki, Y. and Shinozaki, K.	Large scale analysis of Arabidopsis full-length cDNA	Unpublished (2002)	Contact: Motoaki Seki

TITLE Large scale analysis of Arabidopsis full-length cDNA
JOURNAL Unpublished (2002)
CONTACT Motoaki Seki
COMMENT Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyada, Tsukuba, Ibaraki 305-0074, Japan
Tel.: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified plasmid vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES	Location/Qualifiers
source	1. .631

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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
/clone="RAF17-42-H07"
/clone_1ib="RAF17"
/lab_host="DH10B"
/note="Site 1: BamHI; Site 2: SalI; Subtraction Library
The sequence was obtained from samples subjected to
dehydration-treated (1, 2, 5, 10 and 24 hr) and
rehydration-treated (1, 2, 5, 10, and 24 hr after
dehydration treatment)."
BASE COUNT      178 a      114 c      134 g      205 t
ORIGIN

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Query Match	8.2%;	Score 399.8;	DB 9;	Length 631;
Best Local Similarity	99.3%;	Pred. No. 8.1e-66;		
Matches 412;	Conservative	0;	Mismatches 2;	Indels 1; Gaps 1
OY 1	AACCTGCTCTCCGCAACAACAGATCTCTCTCTCCGCGGTACGAGTTTCGTTAAGG	60		
Db				
414	AACCTGCTCTCCGCAACAACAGATCTCTCTCTCCGCGGTACGAGTTTCGTTAAGG	356		
OY 61	ATGTGATTTGTCGAAATAAAATCTGTTCCTTTCTATCATCATCATCATCATAGGACCTA	120		
Db				
355	ATGTGATTTGTCGAAATAAAATCTGTTCCTTTCTATCATCATCATCATCATAGGACCTA	296		
OY 121	ATTGCATCTCTTAAACATCTACTAAATTTCTGGAATGAAAAAACTGAGAAACGCCAAA	180		
Db				
295	ATTGCATCTCTTAAACATCTACTAAATTTCTGGAATGAAAAAACTGAGAAACGCCAAA	236		
OY 181	GAATTCACACAGCATCAGAAAACTAGATAGTTCGTTCGCCGGAGTTCACCAAAACATT	240		
Db				
235	GAATTCACACAGCATCAGAAAACTAGATAGTTCGTTCGCCGGAGTTCACCAAAACATT	176		
OY 241	AGAAAAAATGATACTTACACGAATTCACCAATCTGGAAATTTCTTCCCAAGGCAAG	300		
Db				
175	AGAAAAAATGATACTTACACGAATTCACCAATCTTGTGAAATTTCTTCCCAAGGCAAG	116		

QY 301 CCAATGCTGGCGAGTAAAGAAGAAATTTGGTAACATGACACGCCAATCACAGTGAAGAGAA 360
Db 115 CCATGCTGGCGAGTAAAGAAGAAATTTGGTAACATGACACGCCAATCACAGTGAAGAGAA 56
QY 361 TTGATTTTGTAGTCTCGATTCATCACTACGTGTGTAATACAGAGATGACAGG 415
Db 55 TTGATTTTGTAGTCTCGATTCATCACTATGTTGTAATACAGAGATGACAGG 1

RESULT	4
B18303	
LOCUS	B18303
DEFINITION	B18303 835 bp DNA linear GSS 09-AUG-1997 F24B19-Sp6 IGF Arabidopsis thaliana genomic clone F24B19, DNA sequence.
ACCESSION	B18303
VERSION	B18303.1 GI:2316207
KEYWORDS	GSS.
SOURCE	thale cress.
ORGANISM	Arabidopsis .thaliana

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 835)	Feng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and Ecker, J.	BAC End Sequences at ATGC	Unpublished (1997)	Contact: Ecker J.

TITLE	JOURNAL	COMMENT
BAC End Sequences at ATGC	Unpublished (1997)	
Contact: Ecker J.		
Arabidopsis Thaliana Genome Center		
University of Pennsylvania		
Dept. of Biology, University of Pennsylvania, Philadelphia, PA		
19104		
Tel: 215-898-9384		
Fax: 215-898-8780		
Email: jecker@genome.bio.upenn.edu		
Seq primer: Sp6		
Class: BAC ends		
High quality sequence start: 104		
High quality sequence stop: 116.		

FEATURES	Location/Qualifiers
source	1. .835

BASE COUNT	ORIGIN
187 a	183 c 163 g 258 t 44 others

Query Match	6.18;	Score 299.4;	DB 17;	Length 835;
Best Local Similarity	74.68;	Pred. NO. 8.6e-47;		
Matches 515; Conservative	0;	Mismatches 152;	Indels 23;	Gaps 12;

QY	3280	GCAGAAATTCCTGCAATTTACATAAAGCTATGACTGATGACAAAGGCAAGAGTTCCAGG	3333
Db	118	GCTCGAATTCCTGCAATTTACATAAAGCTATGACTGATGACAAAGGCAAGAGTTCCATG	177
QY	3340	AGGCAAAACGGGAATGTTTGTTGGGCGAAGGCCCGCTAAGAGGTGTCATATATA	3399
Db	178	ATGCAATATCGGAATGTTTGTTGGGCGTGGGANG--GGGCGTCAAAAGGTGTATATATA	236
QY	3400	GGCCCAACTAGCTAGTGAAGCTTAGCTATATTCCTTTTCAAGCTAAACAATTTGATGTG	3455
Db	237	GCCTCACTAGCTAGTGAAGCTTAGCTATATCCCTTTTGAAC-----TAAACTTTNG	289
QY	3460	TATGAATCTCTTGGGCTCTCGGTTTGTGAGATTTGGCGTCGTATCTCAACATC	3519
Db	290	ATTGATATGCTCTCTGCTCTGCGGTGTGGCAATGTGCGCT-TATATCA-----C	344
QY	3520	TGGTAAACTAAACATAGTCTCTCTTTAAACGCTTGGATGATGACACTATTCTACATTATA	3579

Query Match	6.18;	Score 297;	DB 17;	Length 875;
Best Local Similarity	65.4%;	Pred. No. 2.4e-46;		

RESULT 6	AV789413/c	399 bp	mrna	linear	EST 29-MAR-2002
LOCUS	AV789413				
DEFINITION	AV789413	RAFL6	Arabidopsis thaliana	CDNA clone	RAFL06-83-122 3'
ACCESSION	AV789413				
					mrna sequence.


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Db 236 CATTGACACCTTCATCAAGTATCTGTTATGTTGTAACCTATATGACTTCTAT 177
OY 1774 TGGGTAGTATTTGCGATGATGATCTTCATTTTGAATGCTTGTGGATTTA 1833
Db 176 TGGGTAGTATTTGCGATGATGATCTTCATTTTGAATGCTTGTGGATTTA 117
OY 1834 TTTGAGGAACT-----CTGCTTACTAGCATTCTCCATATATATTTTGGCTTTTC 1888
Db 116 TTTAAGATCTAAGCTATTTGCAATGTTAGCAATACATCAATATATCTTTC 59
OY 1889 TCGACATTGGAGTCAAGTTTACTAATGTTCCATTTTGTAGTACCTGT 1940
Db 58 TAGACAGTAGAGGTGATGCTTGTGAAATTCACAGTTAAGTAGTCACT 7

RESULT 8
BE522479/c 313 bp mRNA linear EST 19-MAR-2001
LOCUS M26B4XM Arabidopsis developing seed Arabidopsis thaliana cDNA
DEFINITION clone M26B4 3', mRNA sequence.
ACCESSION BE522479
VERSION BE522479.1 GI:9780457
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 313)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de
Lardya, O., Jaworski, J.G., Ohlrogge, J. and Banning, C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
224 Biochemistry, Michigan State University, East Lansing, MI 48824
, USA
Tel: 517 355 1609
Fax: 517 353 9334
Email: bennings@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.

FEATURES
Source
1..313
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="M26B4"
/clone_id="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 105 a 60 c 53 g 95 t
ORIGIN
Query Match 5.3%; Score 258.8; DB 10; Length 313;
Best Local Similarity 98.9%; Pred. No. 5.3e-39;
Matches 271; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 3978 AAGGTATGGGAATATTTGGAAGCTGATTTGTGAG-AAGTCAATAACAGATCATTCGCGG 4036
Db 274 AAGGTATGGGAATATTTGGAAGCTGATTTGTGAG-AAGTCAATAACAGATCATTCGCGG 215
OY 4037 AATTATGATGTGAACGAAGTCTGTTTCATTTTCTACTTATTTACGTTAATTCGAA 4096
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Db 214 AATTATGATGTGAACGAAGTCTGTTTCATTTTCTACTATTACGTTAATTCGAA 155
OY 4097 CGTTGAATCATCAAAAGACCGTGCCAAACAAATGCAATGATGATGATGATTC 4156
Db 154 CGTTGAATCATCAAAAGACCGTGCCAAACAAATGCAATGATGATGATGATTC 95
OY 4157 TTTTGCTGATTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 4216
Db 94 TTTTGCTGATTTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 35
OY 4217 GATTATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 4250
Db 34 GATTATCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1

RESULT 9
AV820534/c 397 bp mRNA linear EST 01-APR-2002
LOCUS AV820534 RAF11 Arabidopsis thaliana cDNA clone RAF11-10-006 3',
DEFINITION mRNA sequence.
ACCESSION AV820534
VERSION AV820534.1 GI:19862508
KEYWORDS EST.
SOURCE thale cress.
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Eukaryota; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 397)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinozaki, K., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
Large scale analysis of Arabidopsis full-length cDNA (2002b)
Unpublished (2002)
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekic@rcc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
as reported previously (Seki et al., 1998). cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda PLG-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES
Source
1..397
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="RAF11-10-006"
/clone_id="Arabidopsis full-length cDNA"
/tissue_type="seed"
/dev_stage="plants at various developmental stages from
germination to mature seeds"
/lab_host="DH10B"
/note="Site_1: BamHI; Site_2: SalI; subjected to various
treatments (dehydration, cold, high salt, ABA, heat and UV
). Dark-grown plants"

BASE COUNT 139 a 71 c 79 g 108 t
ORIGIN
Query Match 5.3%; Score 258.8; DB 10; Length 397;
Best Local Similarity 98.9%; Pred. No. 5.1e-39;
Matches 271; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

OY 3978 AAGGTATGGGAATATTTGGAAGCTGATTTGTGAG-AAGTCAATAACAGATCATTCGCGG 4036
Db 274 AAGGTATGGGAATATTTGGAAGCTGATTTGTGAG-AAGTCAATAACAGATCATTCGCGG 215
OY 4037 AATTATGATGTGAACGAAGTCTGTTTCATTTTCTACTTATTTACGTTAATTCGAA 4096
|||||

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81 GAATTCACACACACAGCATCAGAAACTAGATCTAGGTTTCGCCGGAGTTACCAAAAACATT 22

Db 21 AGAAAAATCGATACTTACAC 1

RESULT	12
AV810289/c	
LOCUS	AV810289
DEFINITION	421 bp mRNA linear EST 29-MAR-2002 AV810289 RAEF9 Arabidopsis thaliana cDNA clone RAEF09-63-F02 3'
ACCESSION	AV810289
VERSION	AV810289
KEYWORDS	mRNA sequence.
SOURCE	EST. thale cresc.
ORGANISM	Arabidopsis thaliana
	Phylum: Embryophyta; Tracheophyta;

REFERENCE	1 (bases 1 to 421)
AUTHORS	Seki, M., Narusaka, T., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawaji, J., Itoh, M., Ishii, Y.,

TITLE	Large scale analysis of Arabidopsis full-length
JOURNAL	Unpublished (2002)
COMMENT	Contact: Motoaki Seki Plant Functional Genomics Research Group

Email: msek@erc.fiken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda Fd₁ vector (Clontech, Santa Clara, CA) submitted for publication) digested with BamHI and XhoI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.fiken.go.jp/e/Plant/index_e.html) for further details.

FEATURES	Location/Qualifiers
source	1. .421

BASE COUNT	153 a	62 c	91 g	115 t
ORIGIN				

Query Match	4.78;	Score 231;	DB 10;	Length 421;
Best Local Similarity	94.08;	Pred. No. 9.4e-34;		
Matches 251: Conservative	0;	Mismatches 15;	Indels 1;	Gaps 1

3978 AAGGATGGGAATATTGGAAGCTGATTGTGAG - AAGTCAAAATACAGGATCATTTCCGGG 4036

[illegible]

Db 208 AATTTATTTGATTGTAACGAAGTCTTTTTTCTCATTTTCTACTTATTACATTAAATTCGAA 149

4097 CGTTGGAATCATCAAAAGACCGTGCCAAAACAATAATGCAATTGATGCGATAGACATTTC 4156

[illegible]

88 TTTTGGCTGATTGCTATAGGTTTTCAATCTCTAGCTACACTTATGTTATTTCCCTA 29

OY	4217 GATTATCAAGTTAGCCCTGCCGTTTC	4243
Dd	28 GATTATCAAGTTAGCCTTCCCCTTTC	2

RESULT 13					
AV817908/c		410 bp	mRNA	linear	EST 01-APR-2002
LOCUS	AV817908				
DEFINITION	AV817908 Arabidopsis thaliana cDNA clone RAFL09-96-B14 3'				
	mRNA sequence.				
ACCESSION	AV817908				
VERSION	AV817908.1				
KEYWORDS	GI:19859807				
SOURCE	EST.				
ORGANISM	thale cress:				
	Arabidopsis thaliana				

REFERENCE	1 (bases 1 to 410)	Satou, M., Nakajima, M.
AUTHORS	Seki, M., Narusaka, M., Ishida, T., Kamiya, A., Seki, M., Narusaka, M., Ishida, T., Kamiya, A., Satou, M., Nakajima, M.	

TITLE	Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL	Unpublished (2002)
COMMENT	Contact: Motoaki Seki Arabidopsis Research Group National Institute of Advanced Industrial Science and Technology 1-1-1 Higashi, Tsukuba, Ibaraki 305-8565, Japan

Email: mseki@erc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda Fli-1 vector (Garnicki et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES	Location/Qualifiers
source	1. .410

BASE COUNT	139 a	78 c	82 g	111 t
ORIGIN				

Query Match	4.7%;	Score 230.2;	DB 10;	length 410;
Best Local Similarity	97.8%;	Pred. No. 1.3e-33;		
Matches 365;	Conservative	0;	Mismatches 3;	Indels 3;
				Gaps 3

3978 AAGGATATGGGAATATTGGAAGCTGATGTGAG-AAGTCAATACAGGATCATTCGGG 4036

Db 270 AAAGTATGGGAATATTTGGAAGCTGTATTGAGAAGTCAAATACAGGATCATTCCTCCG

310. AATTGTTTAAAGGAGTCTGCTGCTTCATCTTTTCTACTTATTACG-TAATTTCGAA 152

4097 CGTTGGATCATCAAAAGACCGTGCCTAAACAAAATGCAATTGATGCGATGACATTTC 415

Db 151 CGTTGATCATCAAAGACCGTGCCAAACAAAAATGCCAATIGATTCGATAGGCAATC 22

[illegible]

QY 4216 AGATTATCAAGTTAGCTCCGTTTCTAA 4246
 |||||||
 Db 31 AGATTATCAAGTTAGCTCCGTTTCTTA 1

RESULT 14
 AV544837/c 457 bp mRNA linear EST 07-SEP-2000
 LOCUS AV544837 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
 DEFINITION cDNA clone R260h02F 3', mRNA sequence.
 ACCESSION AV544837
 VERSION AV544837.1 GI:8716251
 KEYWORDS EST.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 457)
 AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
 JOURNAL DNA Res. 7, 175-180 (2000)
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
 source
 1. .457
 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="R260h02F"
 /clone_1b="Arabidopsis thaliana roots Columbia"
 /tissue_type="roots"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 156 a 86 c 92 g 122 t 1 others
 ORIGIN

Query Match 4.6%; Score 224.8; DB 10; Length 457;
 Best Local Similarity 98.8%; Pred. No. 1.4e-32;
 Matches 237; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 3978 AAGGTATGGAATATTTGAAGCTGATTGTGAG-AAGTCAATACAGATCATTCGGG 4036
 |||||||
 Db 240 AAGGTATGGAATATTTGAAGCTGATTGTGAG-AAGTCAATACAGATCATTCGGG 181

QY 4037 AATTATGATTGTAACGAAGTCTGTTGTCATATTTCTACTATTATGCTTAATTCGA 4096
 |||||||
 Db 180 AATTATGATTGTAACGAAGTCTGTTGTCATATTTCTACTATTATGCTTAATTCGA 121

QY 4097 CGTTGAAATCATCAAAAGACCGTGCACAAACAAATGCAATTTGATGAGATTC 4156
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 Db 120 CGTTGAAATCATCAAAAGACCGTGCACAAACAAATGCAATTTGATGAGATTC 61

QY 4157 TTTTGGCTGATTGTAATAGGTTTCAATCTCTAGCTTATGTTATTTCCCTA 4216
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 Db 60 TTTTGGCTGATTGTAATAGGTTTCAATCTCTAGCTTATGTTATTTCCCTA 1

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 LOCUS AV553366 Arabidopsis thaliana roots Columbia Arabidopsis thaliana
 DEFINITION cDNA clone R260h02R 5', mRNA sequence.
 ACCESSION AV553366
 VERSION AV553366.1 GI:8724779
 KEYWORDS EST.

SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE 1 (bases 1 to 529)
 AUTHORS Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
 TITLE A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
 JOURNAL DNA Res. 7, 175-180 (2000)
 COMMENT Contact: Erika Asamizu
 The First Laboratory for Plant Gene Research
 Kazusa DNA Research Institute
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
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 /organism="Arabidopsis thaliana"
 /strain="Columbia"
 /db_xref="taxon:3702"
 /clone="R260h02R"
 /clone_1b="Arabidopsis thaliana roots Columbia"
 /tissue_type="roots"
 /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 128 a 113 c 116 g 172 t 1
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 Best Local Similarity 100.0%; Pred. No. 1.9e-32;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

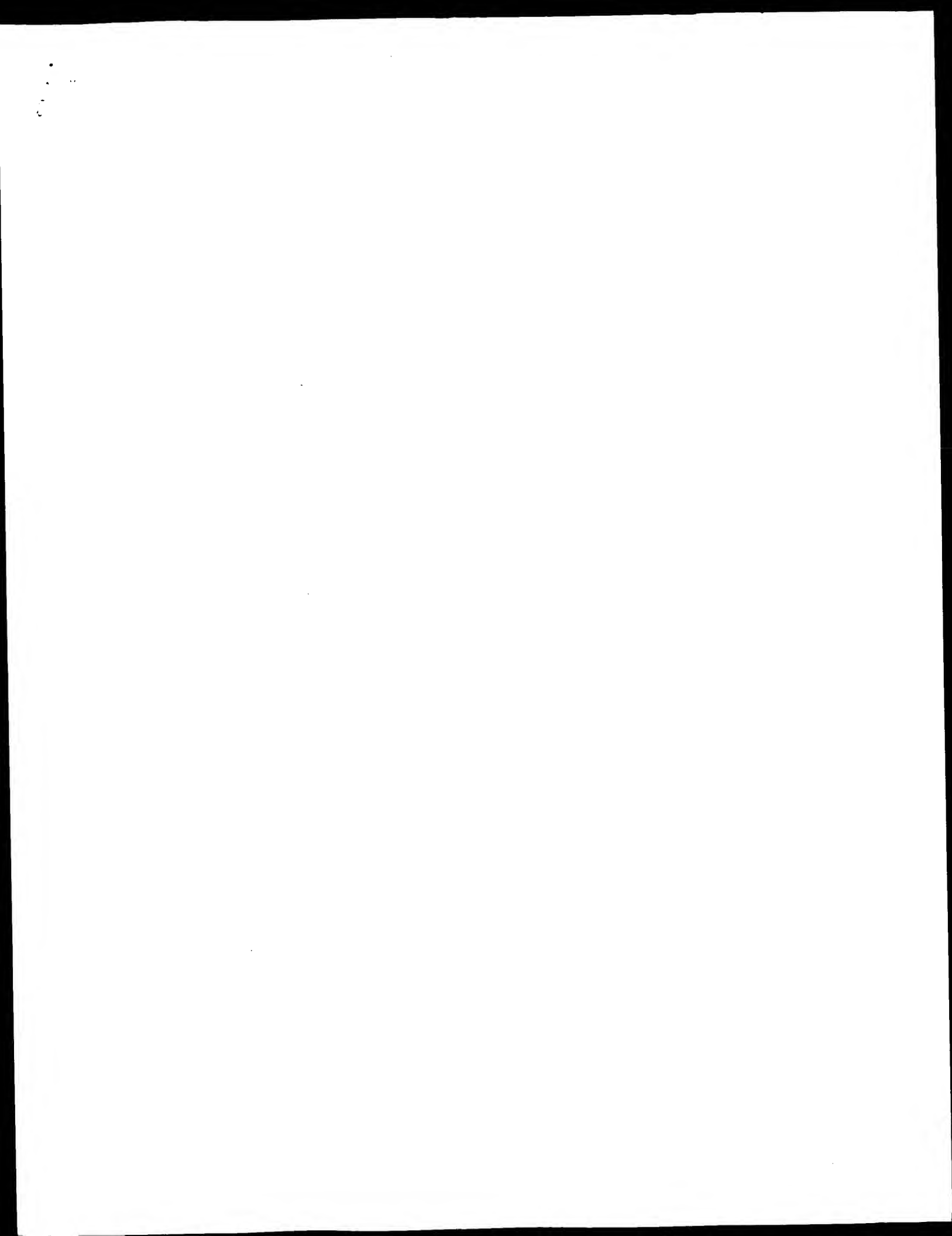
QY 1049 ATGTACACATGTTGATCATGATGAGTGTCTGTTACTCAAGACCTTGGCTTTTGGGA 1108
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QY 1109 GAATGAGTTCAAGACTTATCAACATATGCGCAAGACCCACTTGTATGCTTGGAAAT 1168
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 Db 173 GAATGAGTTCAAGACTTATCAACATATGCGCAAGACCCACTTGTATGCTTGGAAAT 232

QY 1169 TATATTTGCTATGAGACATTTGAGCTATTTCTGAGCTGCTTGGTAAAGAGT 1228
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 Db 233 TATATTTGCTATGAGACATTTGAGCTATTTCTGAGCTGCTTGGTAAAGAGT 292

QY 1229 TGAGGTCCAAATATCTCCACCGGAAACGACAGTTTCAAGG 1272
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 Db 293 TGAGGTCCAAATATCTCCACCGGAAACGACAGTTTCAAGG 336

Search completed: January 16, 2003, 15:15:54
 Job time : 6246 secs



1109 GAATGACITCAAGACTTATCACATATGGCCCAAGACCCACTTTGATTCCTTGAAAT 1166

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Db 222 GAATGAGTTCACAGACTATCAACATATGCGACAGACCACCTTATGTTGGAAT 281
QY 1169 TATATTTTGTATGAGACATTTAAGCTATCTTCAGCGCTTCGCCGTAAGAGT 1228
Db 282 TATATTTTGTATGAGACATTTAAGCTATCTTCAGCGCTTCGCCGTAAGAGT 341
QY 1229 TGAGGTCACAATATCTCCAGCCGGAACCGACGATTACAGG 1272
Db 342 TGAGGTCACAATATCTCCAGCCGGAACCGACGATTACAGG 385

RESULT 2
US-08-931-047-1

; Sequence 1, Application US/08931047
; Patent No. 5965417
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA sequence coding for a protein of
; TITLE OF INVENTION: A. thaliana having a delta-5,7 sterol,
; TITLE OF INVENTION: delta-7 reductase activity, delta7-Red
; TITLE OF INVENTION: protein, production process, strains
; TITLE OF INVENTION: of transformed yeasts, uses.
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/931.047
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9501723
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA: FR 9506517
; APPLICATION NUMBER: FR 9506517
; FILING DATE: 01-JUN-1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1496 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 76..1365
; US-08-931-047-1

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Best Local Similarity 100.0%; Pred. No. 5.1e-47;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1049 ATGTACACATGTTTCATCAGAGTGTCTTACTACAGACTTTGGCTTTGGGA 1108
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QY 1109 GAATGAGTTCACAGACTATCAACATATGCGACAGACCACCTTATGTTGGAAT 1168
Db 222 GAATGAGTTCACAGACTATCAACATATGCGACAGACCACCTTATGTTGGAAT 281
QY 1169 TATATTTTGTATGAGACATTTAAGCTATCTTCAGCGCTTCGCCGTAAGAGT 1228
Db 282 TATATTTTGTATGAGACATTTAAGCTATCTTCAGCGCTTCGCCGTAAGAGT 341
QY 1229 TGAGGTCACAATATCTCCAGCCGGAACCGACGATTACAGG 1272
Db 342 TGAGGTCACAATATCTCCAGCCGGAACCGACGATTACAGG 385

RESULT 3
US-08-783-202-1

; Sequence 1, Application US/08783202
; Patent No. 5989881
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA sequence coding for a protein of A.
; TITLE OF INVENTION: thaliana having a delta-5,7 sterol, delta-7 reductase
; TITLE OF INVENTION: activity, delta7-Red protein, production process, strains
; TITLE OF INVENTION: of transformed yeasts, uses.
; NUMBER OF SEQUENCES: 31
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/783.202
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9501723
; FILING DATE: 15-FEB-1995
; PRIOR APPLICATION DATA: FR 9506517
; APPLICATION NUMBER: FR 9506517
; FILING DATE: 01-JUN-1995
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1496 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 76..1365
; US-08-783-202-1

Query Match 4.6%; Score 224; DB 2; Length 1496;
Best Local Similarity 100.0%; Pred. No. 5.1e-47;
Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 162 ATGTACACATGTTTCATCAGAGTGTCTTACTACAGACTTTGGCTTTGGGA 221
QY 1109 GAATGAGTTCACAGACTATCAACATATGCGACAGACCACCTTATGTTGGAAT 1168
Db 222 GAATGAGTTCACAGACTATCAACATATGCGACAGACCACCTTATGTTGGAAT 281
QY 1169 TATATTTTGTATGAGACATTTAAGCTATCTTCAGCGCTTCGCCGTAAGAGT 1228
Db 282 TATATTTTGTATGAGACATTTAAGCTATCTTCAGCGCTTCGCCGTAAGAGT 341
QY 1229 TGAGGTCACAATATCTCCAGCCGGAACCGACGATTACAGG 1272
Db 342 TGAGGTCACAATATCTCCAGCCGGAACCGACGATTACAGG 385

RESULT 4
US-09-443-041A-19

; Sequence 19, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omlayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:

;; CURRENT APPLICATION NUMBER: US/09/443,041A
;; CURRENT FILING DATE: 1999-11-18
;; PRIOR APPLICATION NUMBER: 60/109,283
;; PRIOR FILING DATE: 1998-11-20
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 19
;; LENGTH: 1646
;; TYPE: DNA
;; ORGANISM: Glycine max
US-09-443-041A-19

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Best Local Similarity 67.3%; Pred. No. 1.3e-17;
Matches 152; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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QY 1109 GAATGAGTTCCAGACTTATCAACATATGAGCCAAAGCCACCTTGTGTAAGAAAT 1168
DB 205 GAATGAGTTCCAGAGGTTGTATCAATATATGAGCCCAACCCCACTCCACCGCTTCAAAAT 264
QY 1169 TATATTTGCTATGAGCATTTGAAGCTATTTCTTCACTGCTTCTGCTGTAAGAGT 1228
DB 265 CATTGACGTTATGCTGCTGATTTGAGGAGCATTCAGCTTCTTCCCGGAAACCGT 324
QY 1229 TGAGGTCCTCATATCTCCAGCGGAAACCGACGCTTCAAGSTA 1274
DB 325 TTACGGCCCTATTTCTCCACCGGACGACGCTGTCAAGGCA 370

RESULT 5
US-09-443-041A-5
;; Sequence 5, Application US/09443041A
;; Patent No. 6465717
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Orozco, Buddy
;; APPLICANT: Rafalski, Antoni
;; APPLICANT: Shen, Jennie
;; TITLE OF INVENTION: Sterol Metabolism Enzymes
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/09/443,041A
;; CURRENT FILING DATE: 1999-11-18
;; PRIOR APPLICATION NUMBER: 60/109,283
;; PRIOR FILING DATE: 1998-11-20
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 5
;; LENGTH: 587
;; TYPE: DNA
;; ORGANISM: Glycine max
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (282)
;; OTHER INFORMATION: any nucleotide
;; NAME/KEY: unsure
;; LOCATION: (335)
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;; LOCATION: (355)
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;; OTHER INFORMATION: any nucleotide
US-09-443-041A-5

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Best Local Similarity 62.4%; Pred. No. 7.9e-14;
Matches 141; Conservative 0; Mismatches 85; Indels 0; Gaps 0;
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DB 138 ATGTACACATGTTCTCTGCTGAGGATGTTCTTCCAGCATTTCCATTTTAAAGCA 197
QY 1109 GAATGAGTTCCAGACTTATCAACATATGAGCCAAAGCCACCTTGTGTAAGAAAT 1168
DB 198 GAATGAGTTCCAGAGGTTGTATCAATATATGAGCCCAACCCCACTCCACCGCTTCAAAAT 257
QY 1169 TATATTTGCTATGAGCATTTGAAGCTATTTCTTCACTGCTTCTGCTGTAAGAGT 1228
DB 258 CATTGACGTTATGCTGCTGATTTGAGGAGCATTCAGCTTCTTCCCGGAAACCGT 317
QY 1229 TGAGGTCCTCATATCTCCAGCGGAAACCGACGCTTCAAGSTA 1274
DB 318 TTACGGCCCTATTTCTCCACCGGACGACGCTGTCAAGGCA 363

RESULT 6
US-09-443-041A-17
;; Sequence 17, Application US/09443041A
;; Patent No. 6465717
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Orozco, Buddy
;; APPLICANT: Rafalski, Antoni
;; APPLICANT: Shen, Jennie
;; TITLE OF INVENTION: Sterol Metabolism Enzymes
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/09/443,041A
;; CURRENT FILING DATE: 1999-11-18
;; PRIOR APPLICATION NUMBER: 60/109,283
;; PRIOR FILING DATE: 1998-11-20
;; NUMBER OF SEQ ID NOS: 33
;; SOFTWARE: Microsoft Office 97
;; SEQ ID NO 17
;; LENGTH: 1870
;; TYPE: DNA
;; ORGANISM: Oryza sativa
US-09-443-041A-17

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Best Local Similarity 77.3%; Pred. No. 4.3e-13;
Matches 109; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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QY 2466 CTGATGCTGCTATGATGATCAAAATTTCTTGTGGAAGCTGTTATTTGAACCATG 2525
DB 810 TTGATGTTGATCTATGATCAACCAAGTTCTTGTGGAATCTGATATGCTGACATATG 869
QY 2526 GACATTCGATGACGAGGT 2546
DB 870 GACATTCGATGATGAGCT 890

RESULT 7
US-09-443-041A-21
;; Sequence 21, Application US/09443041A
;; Patent No. 6465717
;; GENERAL INFORMATION:
;; APPLICANT: Famodu, Omolayo O.
;; APPLICANT: Orozco, Buddy
;; APPLICANT: Rafalski, Antoni
;; APPLICANT: Shen, Jennie
;; TITLE OF INVENTION: Sterol Metabolism Enzymes
;; FILE REFERENCE:
;; CURRENT APPLICATION NUMBER: US/09/443,041A
;; CURRENT FILING DATE: 1999-11-18

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NAME/KEY: misc_feature
LOCATION: 1..260
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; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear

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; STREET: 620 Newport Center Drive 16th Floor
; City: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israel, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-0176
; TELEFAX: (619) 235-8550
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
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Best Local Similarity 46.7%; Pred. No. 0.13;
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DB 15928 ATTTTATTTTATTCATTAAATTTTAAATTTTATTTTATTTAATTAATTTTATT 15869
QY 1462 AAGTTCGACGACCTGTTGTTGTTAAAGTATGTTACGATCTGTAAGCTTGATT 1521
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QY 1522 TGCATTCGTAT-----GATCACTGGGGAATATTTTGGGACATTAATTTGG 1576
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QY 1577 TTCAATATTTGTTGTTGTTGTTACATAAAGTATGATGATGATGATGATGATC 1636
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DB 15748 TGATATATTTTATTTAATTAATTTTATTTTATTTTATTTTATTTAATTAAT 15689
QY 1637 TTTGTTTCTAGTCTATTTTGTAGAAATTTGACCTTTTGTGCTAAACTTATT 1696
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DB 15688 TTTTATTTTATTTAATTTTATTTTATTTTATTTTATTTTATTTAATTAAT 15629
QY 1697 TTTTCTTGACAGGCGCATGTTGACCTTCATCAAGTACTGCTTCATGTTGTAAC 1756
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DB 15628 TTTTATTTTATTTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 15570
QY 1757 TAAATATGACTCTATTTGATGATGATGATGATGATGATGATGATGATGATG 1816
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DB 15569 TATCAAAATTTATTTTATTTAATTTTATTTTATTTTATTTTATTTTATTTT 15510
QY 1817 TTGCTTGTGGATTTATTTGAGAACTGCTGCTTACAGCAACT 1863
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RESULT 15
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; Sequence 1, Application US/09443041A
; Patent No. 6465717

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; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Zea mays
; US-09-443-041A-1

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Query Match          0.98: Score 45.6; DB 4; Length 624;
Best Local Similarity 71.4%; Pred. No. 0.037;
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QY 675 CGGAGACTGTACATCTCCGATCGTTACTTACGATCGATGTTATCGCTTCGCTTCT 734
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DB 140 CGGTTACAGTGCACCTCGGCGGTGTCACCTACACCTGCATCGCTCGCTCTCTCTCT 199
QY 735 GTCACCTTTTCGTCATCTCTCTCT 758
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DB 200 GCCCGCCCTTCGTCATCTCTCTCT 223

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Job time : 240 secs

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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: gb_pl : *

9: gb_pr : *

10: gb_ro : *

11: gb_sts : *

12: gb_sy : *

13: gb_un : *

14: gb_vi : *

15: em_da : *

16: em_fun : *

17: em_hum : *

18: em_in : *

19: em_mu : *

20: em_om : *

21: em_or : *

22: em_ov : *

23: em_pat : *

24: em_ph : *

25: em_pl : *

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31: em_hlg_inv : *

32: em_hlg_other : *

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4868	99.8	4880	8 AF239701	AF239701 Arabidops
2	4750	97.4	105733	8 AC012561	AC012561 Arabidops
3	251.8	5.2	1547	8 AY09589	AY09589 Arabidops
4	237.4	4.9	1194	4 AY085063	AY085063 Arabidops
5	224	4.6	1496	6 AY2625	AY2625 Arabidops
6	224	4.6	1496	6 AR079111	AR079111 Sequence 1
7	224	4.6	1496	6 AR088377	AR088377 Sequence 1
8	224	4.6	1497	8 AT049398	AT049398 Arabidops
9	135.6	2.8	125348	2 AP004850	AP004850 Oryza sat
10	135.6	2.8	178138	2 AP005514	AP005514 Oryza sat
11	75	1.5	143585	2 AC013349	AC013349 Homo sapi
12	69.2	1.4	9539	6 AX277889	AX277889 Sequence
13	69.2	1.4	9539	6 AX323566	AX323566 Sequence
14	68.8	1.4	6668	6 AX346599	AX346599 Sequence
15	67.2	1.4	166544	2 AC125605	AC125605 Homo sapi
16	66.8	1.4	70511	2 AC091083	AC091083 Homo sapi
17	66.6	1.4	7218	6 I66494	I66494 Sequence 14
18	66.4	1.4	156550	2 AC015830	AC015830 Homo sapi
19	65.6	1.3	1141	6 AX083744	AX083744 Sequence
20	65.6	1.3	157362	2 CNO580CAU	AL844497 Oryza sat
21	65.4	1.3	86581	2 AC106497	AC106497 Rattus no
22	65.4	1.3	176663	2 AC117848	AC117848 Rattus no
23	64.6	1.3	114897	2 AP003624	AP003624 Oryza sat
24	64.2	1.3	34769	6 AX251533	AX251533 Sequence
25	63.8	1.3	6644	6 E23356	E23356 Virus vecto
26	63.8	1.3	7372	6 E23357	E23357 Virus vecto
27	63.8	1.3	7797	6 E23355	E23355 Virus vecto
28	63.8	1.3	7996	6 E23359	E23359 Virus vecto
29	63.8	1.3	14006	6 AX346860	AX346860 Sequence
30	63.8	1.3	349980	6 AX344559	AX344559 Sequence
31	63.8	1.3	349980	6 AX344570	AX344570 Sequence
32	63.8	1.3	349980	6 AX344571	AX344571 Sequence
33	63	1.3	210105	2 AC125948	AC125948 Rattus no
34	62.8	1.3	83440	2 AC024285	AC024285 Homo sapi
35	62.8	1.3	170568	2 AC107605	AC107605 Rattus no
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37	62	1.3	538	8 AF117293	AF117293 Castanea
38	61.8	1.3	349980	6 AX344566	AX344566 Sequence
39	61.6	1.3	18598	6 AX345288	AX345288 Sequence
40	61.4	1.3	33068	3 AC115682	AC115682 Dictyoste
41	61.4	1.3	131271	2 AC015927	AC015927 Homo sapi
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ALIGNMENTS

RESULT 1

AF239701

LOCUS Arabidopsis thaliana sterol delta7 reductase (DWARF5) gene,

DEFINITION complete cds.

ACCESSION AF239701

VERSION AF239701.1 GI:7542560

KEYWORDS

SOURCE

ORGANISM

thale cress.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidops.

REFERENCE

1 (bases 1 to 4880)

Choe,S., Tanaka,A., Noguchi,T., Fujioke,S., Takatsuto,S.,

TITLE
 Lesions in the sterol delta reductase gene of Arabidopsis cause
 dwarfism due to a block in brassinosteroid biosynthesis
 JOURNAL
 Plant J. 21 (5), 431-443 (2000)
 MEDLINE
 20223137
 PUBMED
 10758495
 REFERENCE
 2 (bases 1 to 4880)
 AUTHORS
 Choe, S.
 TITLE
 Direct Submission
 Submitted (27-FEB-2000) Plant Sciences, University of Arizona,
 Forbes hall 303, Tucson, AZ 85721, USA
 JOURNAL
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 VERSION
 AC012561.2 GI:6227026
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 ORGANISM
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 Arabidopsis thaliana.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eustosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 105733)
 REFERENCE
 AUTHORS
 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P.,
 Gonzalez, A., Kremetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S.,
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 2 (bases 1 to 105733)
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 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
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 Direct Submission
 Submitted (30-OCT-1999) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 3 (bases 1 to 105733)
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 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
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 Submitted (04-NOV-1999) DNA Sequencing and Technology Center,
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 USA
 4 (bases 1 to 105733)
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 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A.
 and Davis, R.W.
 Direct Submission
 Submitted (26-JUL-2000) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 5 (bases 1 to 105733)
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 AUTHORS
 Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
 Altafi, H., Nguyen, M., Lam, B., Southwick, A., Ecker, J., Theologis, A.
 and Davis, R.W.
 Direct Submission
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 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 On Nov 4, 1999 this sequence version replaced gi:6143852.
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FEATURES
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 Db 95242 AACTCAGCATATATCAAGTTGACTTCACTTTTACATTAATGGTGTTCGAGATC 95301
 |||||||
 QY 4495 CACAAAGTACATATACAGTTTTCACAAATGATGATCTTTATTTTATTTTCTT 4554
 |||||||
 Db 95302 CACAAAGTACATATACAGTTTTCACAAATGATGATCTTTATTTTATTTTCTT 95361
 |||||||
 QY 4555 GGTCAACATACATATTCATTCACACTTTTAAACGAGAGTCCCTCCAGTGAGATATACA 4614
 |||||||
 Db 95362 GGTCAACATACATATTCATTCACACTTTTAAACGAGAGTCCCTCCAGTGAGATATACA 95421
 |||||||
 QY 4615 CAAAAAGTACGAGAGCAAAATGCTCAACAAAAAGCATTAAGAGGAGCTCAGAGCT 4674
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 Db 95422 CAAAAAGTACGAGAGCAAAATGCTCAACAAAAAGCATTAAGAGGAGCTCAGAGCT 95481
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 QY 4675 CAACCGAGTACGAGAGCAAAATGCTTAAACAGAACATCATTTACTTCTGAGGCG 4734
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 Db 95482 CAACCGAGTACGAGAGCAAAATGCTTAAACAGAACATCATTTACTTCTGAGGCG 95541
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 QY 4735 TCTTCGTACCAAGCTCTTCAGCAAAATTTGATTTCTATTTTGGATATCATGATCTA 4794
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 Db 95542 TCTTCGTACCAAGCTCTTCAGCAAAATTTGATTTCTATTTTGGATATCATGATCTA 95601
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 QY 4795 ACTTCAAGTTTTTAAATACAAAAACTTACATCTCTAATTTTGAATCAAGCT-AAACA 4853
 |||||||
 Db 95602 ACTTCAAGTTTTTAAATACAAAAACTTACATCTCTAATTTTGAATCAAGCT-AAACA 95661
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 QY 4854 AATTTCATCTAAAAACATTTTACTG 4879
 |||||||
 Db 95662 AATTTCATCTAAAAACATTTTACTG 95687
 |||||||

RESULT 3
 LOCUS AY099589 1547 bp mRNA linear PLN 06-MAY-2002
 DEFINITION Arabidopsis thaliana sterol delta7 reductase (Atlg50430) mRNA,
 complete cds.
 ACCESSION AY099589
 VERSION AY099589.1 GI:20466245
 KEYWORDS FLI CDNA.
 SOURCE Arabidopsis thaliana.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 1547)
 Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M.,
 Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H.,
 Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A.,
 Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K.,
 Sakano,H., Sakurai,T., Satou,M., Seki,M., Shim,P., Yamada,K.,
 Shinzeki,K., Ecker,J., Theologis,A. and Davis,R.W.
 Direct Submission
 Submitted (24-APR-2002) DNA Sequencing and Technology Center,
 Stanford University, 855 California Avenue, Palo Alto, CA 94304,
 USA
 COMMENT e-mail for correspondence: arabsequence.stanford.edu

RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL CDNA (RAFL CDNA : 'RIKEN
 Arabidopsis Full-Length CDNA') : Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinzeki,K.
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL CDNA's : Nguyen,M.,
 Southwick,A., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J.,

Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K.,
 Kim,C., Lin,J., Liu,S.X., Pham,P.K., Sakano,H., Shim,P.,
 Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
 Nguyen,M. (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed
 equally to this work. Shinzeki,K. (RIKEN GSC) and Davis,R.W.
 (SSP/Stanford) contributed equally to this work as PIs.
 Location/Qualifiers
 1..1547
 /organism="Arabidopsis thaliana"
 /db_xref="taxon:3702"
 /chromosome="1"
 /clone="RAFL09-63-F02 (R24741)"
 /note="This clone is in plasmid
 ecotype: Columbia"
 1..1547
 /gene="Atlg50430"
 /note="P11F12.21"
 52..1350
 /gene="Atlg50430"
 /codon_start=1
 /product="sterol delta7 reductase"
 /protein_id="AA020440.1"
 /db_xref="GI:20466246"
 /translation="MAETVHSPVIVYASMLSLAECPPVILMTWMHODGSVTQTE
 GFPEWNGVGLINIMPRPLIAKKIFCGAEPALIDLPKREGLSPGNRPVY
 KANGLAAYEVTLATVGLWMFGIFNPAIDHGEFSLIFGSEFVLYIKGVA
 PSSSDSGCNLIIDFYWGMEIKPRIGSPDIKIFGSEFGMSMAVLAIVICROYE
 INKVSQDSMLVNTIIMLVYTKPEPMAGVWNTMDIAHRAGFYICWGLVWVPSVT
 SPQMTLVNHEVEIGTOLATIIYLVAGLICITINDCDROERRRIRNGKLVVGRAPSK
 IVASVTTSGEYTSILNLSGWMGLARHHEHYVEIISAFETWVPALFDFNLAIFYVIF
 LTLFLDRAKRDDRCRSKGYKWKLYCKEYKVRILIPGTY"
 BASE COUNT 399 a 311 c 345 g 492 t
 ORIGIN
 Query Match 5.28; Score 251.8; DB 8; Length 1547;
 Best Local Similarity 98.9%; Pred. No. 2,9e-39;
 Matches 264; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 QY 3978 AAGGATGCGAAATATTGGAAGCTGTATTGTGAG-AGGTCAATACAGATCCGGG 4036
 |||||||
 Db 1281 AAGATATGGAAATATTGGAAGCTGTATTGTGGAAGATCAATACAGATCCGGG 1340
 |||||||
 QY 4037 AATTATGATTTGTACGAAAGCTGTGTTCTCTCATTTTCTACTTATTAGCTTAATCGAA 4096
 |||||||
 Db 1341 AATTATGATTTGTACGAAAGCTGTGTTCTCTCATTTTCTACTTATTAGCTTAATCGAA 1400
 |||||||
 QY 4097 CGTTGGAATCATCAAAAGACCGTCCAAACAAAAATGCAATTTGATGCGATAGACATTC 4156
 |||||||
 Db 1401 CGTTGGAATCATCAAAAGACCGTCCAAACAAAAATGCAATTTGATGCGATAGACATTC 1460
 |||||||
 QY 4157 TTTGCGATTTGTATGCTATAGGTTTTCACAAATCTAGCTAGCTATGATTTCCCTA 4216
 |||||||
 Db 1461 TTTGCGATTTGTATGCTATAGGTTTTCACAAATCTAGCTAGCTATGATTTCCCTA 1520
 |||||||
 QY 4217 GATTATCAAAAGTTAGCCGCGCTTTTC 4243
 |||||||
 Db 1521 GATTATCAAAAGTTAGCCGCGCTTTTC 1547
 |||||||

RESULT 4
 LOCUS AY085063/c 1194 bp mRNA linear PLN 21-JUN-2002
 DEFINITION Arabidopsis thaliana clone 126074 mRNA, complete sequence.
 ACCESSION AY085063
 VERSION AY085063.1 GI:21403773
 KEYWORDS FLI CDNA.
 SOURCE thale cress.
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 1194)

AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N., Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.	Full-length messenger RNA sequences greatly improve genome annotation	Genome Biol. (2002) In press	2 (bases 1 to 1194)	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.	Full-length cDNA from Arabidopsis thaliana unpublished	3 (bases 1 to 1194)	Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and Feldmann,K.	Direct Submission	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Lwr ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.	

[illegible]

QY	301	CGATTCTCTGCGGAGTAAAGAAATGGTAAACATATGACGCGGAATCAGAGTAAAGAA	360
Db	149	CCATTCTCTGCGGAGTAAAGAAATGGTAAACATATGACGCGGAATCAGAGTAAAGAA	90
QY	361	TTTGAAATTTGTATGTCGATTCATCATATGTGTGAATACAGAGATGCAAGATCTT	420
Db	89	TTTGAAATTTGTATGTCGATTCATCATCATATGTGTGAATACAGAGATGCAAGATCTT	30
QY	421	TTGAGGGTTGAGAGAGAAAGACTTAAGAA	449
Db	29	TTGAGGGTTGAGAGAGAAAGACTTAAGAA	1
RESULT 5			
LOCUS	A52625	1496 bp	DNA
DEFINITION	Sequence 1 from Patent EP0727489.	linear	PAT 12-DEC-1997
ACCESSION	A52625		
VERSION	A52625.1	GI:2851857	
KEYWORDS	.		
SOURCE	unidentified.		
ORGANISM	unidentified.		
REFERENCE	1 (bases 1 to 1496)		
AUTHORS	Chenivhesse,X., Duport,C., Lecain,E. and Pompon,D.		
TITLE	DNA sequence coding for an A. thaliana protein with		
JOURNAL	delta-5,7-sterol-delta-7-reductase, the protein, process for the		
COMMENT	production, transformed yeast-strains and use		
	Patient: EP 0727489-A 1 21-AUG-1996;		
	ROUSSEL UCLAF (FR)		
	Other publication SK 18896 961001		

QY	1049	ATGGTACACAAAGCGTCATCAGAGATGGTTCGTTACTACAGACCTTGGCTTCTTTGGGA	1108
DB	162	ATGGTACACAAAGCGTCATCAGAGATGGTTCGTTACTACAGACCTTGGCTTCTTTGGGA	221
QY	1109	GAATGAGATTCAAGGACTTATCAACATATGGCCAAAGCCACTTTGATTCCTTGGAAAT	1168
DB	222	GAATGAGATTCAAGGACTTATCAACATATGGCCAAAGCCACTTTGATTCCTTGGAAAT	281
QY	1169	TATATTTTGCATGAGACATTTGAAGCTATTCTTCAAGCTGCTTTCGCTTGTAAGAGCT	1228

Db 282 TATATTTGCTATGAGCAATTTGAAGCTATTCTTCAGCTGCTTCGCTGTAAGAGCT 341

QY 1229 TGAGGGTCCAAATATCTCCAGCCGGAACCGACAGCTTTCACAG 1272

Db 342 TGAGGGTCCAAATATCTCCAGCCGGAACCGACAGCTTTCACAG 385

RESULT 6

AR079111

LOCUS AR079111 1496 bp DNA linear PAT 31-AUG-2000

DEFINITION Sequence 1 from patent US 5965417.

ACCESSION AR079111

VERSION AR079111.1 GI:10005857

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1496)

AUTHORS Chenivesse,X., Dupont,C., Lecain,E. and Pompon,D.

TITLE Arabidopsis thaliana proteins having .DELTA.-5,7-sterol-.DELTA.-7-reductase activity

JOURNAL Patent: US 5965417-A 1 12-OCT-1999;

FEATURES

source 1..1496

BASE COUNT 399 a 297 c 340 g 460 t

ORIGIN

Query Match 4.6%; Score 224; DB 6; Length 1496;

Best Local Similarity 100.0%; Pred. No. 8.5e-34;

Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1049 ATGCTACACATGCTTCATCAGAGATGCTTCTGTACTCAGACCTTGGCTCTTTGGGA 1108

Db 162 ATGCTACACATGCTTCATCAGAGATGCTTCTGTACTCAGACCTTGGCTCTTTGGGA 221

QY 1109 GAATGAGTTCAGAGCACTTATCAACATATGCGCAAGACCCACTTGTATGCTTGAAGT 1168

Db 222 GAATGAGTTCAGAGCACTTATCAACATATGCGCAAGACCCACTTGTATGCTTGAAGT 281

QY 1169 TATATTTGCTATGAGCAATTTGAAGCTATTCTTCAGCTGCTTCGCTGTAAGAGCT 1228

Db 282 TATATTTGCTATGAGCAATTTGAAGCTATTCTTCAGCTGCTTCGCTGTAAGAGCT 341

QY 1229 TGAGGGTCCAAATATCTCCAGCCGGAACCGACAGCTTTCACAG 1272

Db 342 TGAGGGTCCAAATATCTCCAGCCGGAACCGACAGCTTTCACAG 385

RESULT 7

AR088377

LOCUS AR088377 1496 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 1 from patent US 5989881.

ACCESSION AR088377

VERSION AR088377.1 GI:10015140

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1496)

AUTHORS Chenivesse,X., Dupont,C., Lecain,E. and Pompon,D.

TITLE Nucleic acid molecules encoding delta-5,7-sterol, delta-7 reductase

JOURNAL Patent: US 5989881-A 1 23-NOV-1999;

FEATURES

source 1..1496

BASE COUNT 399 a 297 c 340 g 460 t

ORIGIN

Query Match 4.6%; Score 224; DB 6; Length 1496;

Best Local Similarity 100.0%; Pred. No. 8.5e-34;

Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1049 ATGTCACAAATGATGATCATGAGATGCTGCTTACTCAGACCTTGGCTCTTTGGGA 1108

Db 162 ATGTCACAAATGATGATCATGAGATGCTGCTTACTCAGACCTTGGCTCTTTGGGA 221

QY 1109 GAATGAGTTCAGAGCACTTATCAACATATGCGCAAGACCCACTTGTATGCTTGAAGT 1168

Db 222 GAATGAGTTCAGAGCACTTATCAACATATGCGCAAGACCCACTTGTATGCTTGAAGT 281

QY 1169 TATATTTGCTATGAGCAATTTGAAGCTATTCTTCAGCTGCTTCGCTGTAAGAGCT 1228

Db 282 TATATTTGCTATGAGCAATTTGAAGCTATTCTTCAGCTGCTTCGCTGTAAGAGCT 341

QY 1229 TGAGGGTCCAAATATCTCCAGCCGGAACCGACAGCTTTCACAG 1272

Db 342 TGAGGGTCCAAATATCTCCAGCCGGAACCGACAGCTTTCACAG 385

RESULT 8

ATU49398

LOCUS ATU49398 1497 bp mRNA linear PLN 16-MAY-1996

DEFINITION Arabidopsis thaliana sterol delta-7 reductase (ST7R) mRNA, complete cds.

ACCESSION U49398

VERSION U49398.1 GI:1245181

KEYWORDS

SOURCE Arabidopsis thaliana.

ORGANISM Arabidopsis thaliana.

REFERENCE 1 (bases 1 to 1497)

AUTHORS Lecain,E., Chenivesse,X., Spagnoli,R. and Pompon,D.

TITLE Cloning by metabolic interference in yeast and enzymatic characterization of Arabidopsis thaliana sterol delta-7 reductase

JOURNAL J. Biol. Chem. 271 (18), 10866-10873 (1996)

FEATURES

source 1..1497

gene /organism="Arabidopsis thaliana"

CDS /db_xref="taxon:3702"

1..1497 /tissue-type="full seedling"

76..1368 /gene="ST7R"

1..1497 /note="NADPH dependent; sterol reductase"

1..1497 /product="sterol delta-7 reductase"

1..1497 /protein_id="AAC49278.1"

1..1497 /db_xref="GI:1245182"

1..1497 /translation="MAETVHSPIVTYASMLSLAFPCPPVILMTYMHQDSSVTQTE GFPEWNGVQGLIIMWPRPLDIANKIIFCYGAFAIILQLIPGRVGGPISPAIGNRVY KANGLAAYEVTLATHGLMWFGEJFNPAIVDHLGEIIFGSEFVYLYIKGYA PSSDSGSCGNLIIDPFYCMELVPRIGASPDIVFNCRRGMSMAVLATYCIKOYE INKRVSDSMIVNTILMAYVYTKRFNMEAGCNWMDIAHBRAGFYICMGILVWPSYTT SPQAVLVNHPVEIGTDLATYILVAGILCTIKYDCRQROEFRRIRNGKLVWGRARSK IVASVYTTSGEIKTSLNLSGWLARHFFVYVEILSAFVFWPALDELFLAVFYLT ILLFDRAKRDDDCRSKRYGKWLVEKVKYRIIPGIV"

BASE COUNT 400 a 297 c 340 g 460 t

ORIGIN

Query Match 4.6%; Score 224; DB 8; Length 1497;

Best Local Similarity 100.0%; Pred. No. 8.5e-34;

Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1049	ATGGTACACAAATGGTTCATCAGAGATGGTTCGTCTCTACAGACCTTGGCTTCTTTGGGA	1108
Db	162	ATGGTACACAAATGGTTCATCAGAGATGGTTCGTCTCTCTACAGACCTTGGCTTCTTTGGGA	221
QY	1109	GAATGAGTTCAGGACTTATCATACATATGGCCAAAGACCACCTTGGATGCTTGGAAAT	1168
Db	222	GAATGAGTTCAGGACTTATCATACATATGGCCAAAGACCACCTTGGATGCTTGGAAAT	281
QY	1169	TATATTTTTCCTATGGAGCATTTTGAAGCTATTTCTTACGCTGCTTGCCTGTAAGAACT	1228
Db	282	TATATTTTTCCTATGGAGCATTTTGAAGCTATTTCTTACGCTGCTTGCCTGTAAGAACT	341
QY	1229	TGAGGTCCTCAATATCTCCAGCCGGAAACCGACCTTATCAAGG	1272
Db	342	TGAGGTCCTCAATATCTCCAGCCGGAAACCGACCTTATCAAGG	385
RESULT 9	AP004850	125348 bp	linear
LOCUS	AP004850		HTG 23-MAR-2002
DEFINITION	Oryza sativa (japonica cultivar-group) chromosome 2 clone		
ACCESSION	OJ1342.D02, *** SEQUENCING IN PROGRESS ***		in ordered pieces.
VERSION	AP004850.1		
KEYWORDS	HTG: HTGS, PHASE2.		
SOURCE	Oryza sativa (japonica cultivar-group) (cultivar: Nipponbare) DNA, clone: OJ1342.D02.		
ORGANISM	Oryza sativa (japonica cultivar-group)		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzaceae; Oryza.		
TITLE	1		
JOURNAL	Sasaki, T., Matsumoto, T. and Yamamoto, K.		
AUTHORS	Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC clone: OJ1342.D02		
JOURNAL	Published Only in Database (2002)		
TITLE	2 (bases 1 to 125348)		
JOURNAL	Sasaki, T., Matsumoto, T. and Yamamoto, K.		
COMMENT	Direct Submission		
	Submitted (20-MAR-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan		
	(E-mail: tsasaki@affrc.go.jp, URL: http://rnp.dna.affrc.go.jp/, Tel: 81-298-38-7441, Fax: 81-298-38-7468)		
	The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.		
	NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.		
	* NOTE: This is a 'working draft' sequence.		
	* This sequence will be replaced		
	* by the finished sequence as soon as it is available and		
	* the accession number will be preserved.		
FEATURES	Location/Qualifiers		
SOURCE	1. 125348		
	/organism="Oryza sativa (japonica cultivar-group)"		
	/cultivar="Nipponbare"		
	/db_xref="taxon:39947"		
	/chromosome="2"		
	/clone="OJ1342.D02"		
BASE COUNT	35739 a 27515 c 26919 g 35124 t	51	others.
ORIGIN			
Query Match	2.8%;	Score 135.6;	DB 2; Length 125348;
Best Local Similarity	55.2%;	Pred. No. 9.9e-17;	
Matches 403; Conservative	0;	Mismatches 249;	Indels 78; Gaps 4;
QY	3209	TATGGCTATATCCGTAACGATTCACATATATCCGCTTGTGGAGTGGCAATAT	3268
Db	124567	TGTGATTTGTTGCTTAACGACTTGAATATGATATCTTTAAATTTGTGGAGCTAGACTCT	124626

[illegible]

Agrobiological Sciences, Rice Genome Research Program, Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsukuba@affrc.go.jp, URL: http://rpp.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES

Location/Qualifiers
1..178138
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
/clone="OSJNB40035A24"

BASE COUNT 51522 a 37116 c 36733 g 52716 t 51 others
ORIGIN

Query Match 2.8%; Score 135.6; DB 2; Length 178138;
Best Local Similarity 55.2%; Pred. No. 9.4e-17;
Matches 403; Conservative 0; Mismatches 249; Indels 78; Gaps 4;

DB 24918 TGTGATGTTGTTCTTAACAGTTGAATGATCTGTTAAATGTTGTCAGTACGCTCT
QY 3209 TATGCTATCTCCGATACCTAGCTTCCGCTTTGGTTGCGAGTTGCAATAT 3268
DB 3269 ACATTCCTGTTGAGGATCTGTGATTTACATTAAGTATGATTAACAAGGC 3328
DB 24978 CAATTCCTCTGCTGGAATATTTGATATTAATACATGACTGTGCTGACGCC 25037
QY 3329 AAGAGTTGAGGAGACAAACGGAAATGTTGGTTGGGAGAGCCCGTCAAGTGT 3388
DB 25038 AAGAAATCCGTCGACAAATGGAATGCTCAATATGGGCAAGCTCATTAAGTTG 25097
QY 3389 GATCATATTAAGCCCACTAGCTTAGTACCTATATCTCTTTCAACAGCTAAC 3448
DB 25098 AAGCATTAA-----TATTTAGCTCTTCCAAATTAACAAATAGCA 25138
QY 3449 ATTTGATGATGATGATCTCTGCTGCTCGGTTTGTGAGATGTGCGCTGAT 3508
DB 25139 TGTTTAATACATGCTGAGCTCTTTATTTGGGAGACTTT--AGATTTGCTTCTCTAT 25136
QY 3509 ACTACAACATCTGTAAGCTAACTAGTCTTCTTAACTGCTGATGATGAGACTAT 3568
DB 25197 CAGACTACAATATGAGAAACAAACAGAGCTCTCTGACTCTGATGATTAATATAT 25256
QY 3569 TCTACATTAATAGCAACCAATAAATAGAGCTTGTTCATCATGAGCTTTGAA- 3627
DB 25257 TCGTCATTTCTTCTTACATATGATCAAAAGTATTTGTACCATGTTTGAATAG 25316
QY 3628 -----TGTGAGGTGGGAGTTG 3645
DB 25317 AGGCATGATGCTTTTGAAGTACGACCTCATTTTCCATTTGGACAGGTGGGCTTGT 25376
QY 3646 CTGCTGATTTCCATTAATGTTCTGAGATCTTAAGTCTTTCTTCTGACCGTACCGCTC 3705
DB 25377 CTGCTGATTTCCATTAATGTTCTGAGATCTTAAGTCTTTCTTCTGACCGTACCGCTC 25436
QY 3706 TCTTCATTAAGCAAAATACATCATATTTGCTATATTTGAAGCTCTTCTTGAAGT 3765
DB 25437 TTTTTCATCATGTA-----GCACACCTCATTAACATTTATCTCGACTTT 25482
QY 3766 GAAGCAGCTTAATCATTAATCATTTGTTTAAACGTTCTTGGCATGCTAGCTTACCT 3825
DB 25483 AGCAGAGATGATTAATACATGCTGCTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCT 25542
QY 3826 CATATTTCTCACCCCTCTCTCTTTGATGAGGCAAGAGAGAGATGACCGATGCGGATC 3885

DB 25543 GATCTTTGACCAATATGCTTTCGACCGCTTAAGAGGATGATGACCGATGCTATC 25602
QY 3886 AAGTAAAGCA 3895
DB 25603 AAGTAAAGCA 25612

RESULT 11

AC013349
LOCUS

DEFINITION Homo sapiens clone RP11-22K1, LOW-PASS SEQUENCE SAMPLING.

AC013349
ACCESSION

VERSION AC013349.3 GI:9124043

KEYWORDS HTGS PHASED.

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

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REFERENCE

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REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AC013349 143585 bp DNA linear HTG 13-JUL-2000
Homo sapiens clone RP11-22K1, LOW-PASS SEQUENCE SAMPLING.
AC013349
ACCESSION
AC013349.3 GI:9124043
HTG: HTGS PHASED.
Homo sapiens.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 143585)
Birten, B., Linton, L., Nusbaum, C., and Lander, E.
Homo sapiens, clone RP11-22K1
Unpublished
2 (bases 1 to 143585)
Birten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,
Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donellan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galligan, J., Gardyna, S., Grant, G., Hages, B., Heatford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, D.,
Lehoczky, J., Lieu, C., Locke, K., MacDonald, P., Marquis, N.,
McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Telford, S., Tietzel, A., Vassiliou, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (06-NOV-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jul 13, 2000 this sequence version replaced g1:6910730.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W1BR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: LA134
Center clone name: 22_K_1

* NOTE: This record contains 150 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
* 1 930: contig of 930 bp in length
* 931 1030: gap of 100 bp
* 1031 1955: contig of 925 bp in length
* 1956 2055: gap of 100 bp
* 2056 2959: contig of 904 bp in length
* 2960 3059: gap of 100 bp
* 3060 4006: contig of 947 bp in length
* 4007 4106: gap of 100 bp

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45425	46337:	contig of 913 bp	in length	
46338	46437:	gap of	100 bp	
46438	47340:	contig of 903 bp	in length	
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47441	48330:	contig of 890 bp	in length	
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52330	53186:	contig of 857 bp	in length	
53187	53286:	gap of	100 bp	
53287	54219:	contig of 933 bp	in length	
54220	54319:	gap of	100 bp	
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55207	55306:	gap of	100 bp	
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61251	61350:	gap of	100 bp	
61351	62216:	contig of 866 bp	in length	
62217	62316:	gap of	100 bp	
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63291	64198:	contig of 908 bp	in length	
64199	64298:	gap of	100 bp	
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RESULT 15
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11bpair
HMC_05-III--2002

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DEFINITION	Homo sapiens clone RP11-251H8,	** SEQUENCING IN PROGRESS **	, 9		
ACCSSION	unordered pieces.				
VERSION	ACI25605				
KEYWORDS	ACI25605.2 GI:21693782 HTG: HTGS_PHASE1. human.				
SOURCE ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaralunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbarita,J., Benton,J., Bimaga,K., Blankenburg.K., Bonnin.D., Bouck,J., Bowle.S., Briefe,M., Brown,E., Brown,W., Bryant,N.P., Buahy,C., Butch,P., Burkett,C., Buttell,K.L., Byrd,N.C., Carroll,T.F., Carter,M., Cavazos,S.R., Checko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle-M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-carroll,L., Dedertich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinib.H.B., Donthuwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls.T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frenzt,P., Gabhis T., Gao J., Garcia A., Garner M., Garcia N., Gill R.				

Garrido, J. R., Cuevas, W., Guntaratne, P., Hale, S. S., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlik, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogue, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hult, S., Hume, J., Jackson, L. E., Karlsson, B., Jia, Y., Johnson, R., Jolivet, S., Joudas, S., Karlsson, E., Kelly, S., Khan, J., King, L., Korvach, J., Kovar, C., Kratochvil, J., Kureshi, A., Landry, N., Leal, B., Lewis, L. C., Lewis, L. L. J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louiseged, H., Lozada, R. J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Mareshwar, M., Mapa, P., Martin, R., Martindale, A., Mathew, E., Massey, E., Mathney, E., McLeod, M. P., Meador, M., Mel, G., Metker, M., Miner, G., Mitchell, Z., Mitchell, T., Mohabath, K., Morgan, M., Morris, S., Moser, M., Neel, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokemkwo, S., Oguh, M., Okunodu, N., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rivers, M., Rojas, A., Rojurokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shoochari, N., Sisson, I., Sodergren, E., Sotnik, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabori, P., Tameritsa, D., Tameritsa, K., Tang, H.,

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 15:16:02 ; Search time 194 Seconds
(without alignments)
11213.358 Million cell updates/sec

Title: US-09-817-774-30

Perfect score: 4879

Sequence: 1 aactgtctctctccacaa.....atctaaacaatttactg 4879

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 393868 seqs, 222934149 residues 787736

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications - NA : *

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	4866.4	99.7	4880	10	US-09-817-774-38
7	4866.4	99.7	4880	10	US-09-817-774-40
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14	58.8	1.2	529	10	US-09-983-965-2109
15	55.6	1.1	446	10	US-09-960-352-3400
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24	47.4	1.0	341	10	US-09-960-352-12302	Sequence 12302, A
25	47.4	1.0	408	10	US-09-960-352-1221	Sequence 1221, A
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RESULT 1

US-09-817-774-30

Sequence 30, Application US/09817774

Patent No. US2002012011A1

GENERAL INFORMATION:

APPLICANT: CHOE, Sunghwa

TITLE OF INVENTION: Dwf5 MUTANTS

FILE REFERENCE: 2225-0020 / 91020.002

CURRENT FILING DATE: 2001-03-26

PRIOR APPLICATION NUMBER: 60/192,202

PRIOR FILING DATE: 2000-03-27

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 30

LENGTH: 4879

TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE:

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LOCATION: (671)..(757)

OTHER INFORMATION: dwf5-1

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Db	1501	CAGGTTGGAAATCTCAACCCCTCAATTTGTAATGATCACTGGGTGAAAAATTTTGGCC	1560
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Db	1681	TTGCTAAACCTATTTTCTTGTGTAAGGGGCATGTTGACCTTCATCAAGTGACTCT	1740
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QY	1801	CTCATCTTTTTGAAATTTGGTTGGGAAATTAATTGAGAACTCTGGGCTTACAGCA	1860
Db	1801	CTCATCTTTTTGAAATTTGGTTGGGAAATTAATTGAGAACTCTGGGCTTACAGCA	1860

Qy	1861	TCCTCATATAATTTTGGCTTTCTTCGCACTTTGGAGGTCAAGTTTCACTAAAGTT	1920
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Qy	1921	TCCAATTTTAGTAGACCTGTAAACGGAAATGTTCTTAGCAGTATTATCTTTTATTGAT	1980
Db	1921	TCCAATTTTAGTAGACCTGTAAACGGAAATGTTCTTAGCAGTATTATCTTTTATTGAT	1980
Qy	1981	TTAGTACAAAGAAACCTAGTTTGGTGTGAATGTCTGTGGGTAAAGAAAGAACAAAGTA	2040
Db	1981	TTAGTACAAAGAAACCTAGTTTGGTGTGAATGTCTGTGGGTAAAGAAAGAACAAAGTA	2040
Qy	2041	TGCAGTAGTATTATATAACATATACAGTTGAGATCTCTCTCAGCATGTACTCTTTGCT	2100
Db	2041	TGCAGTAGTATTATATAACATATACAGTTGAGATCTCTCTCAGCATGTACTCTTTGCT	2100
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Db	2101	CCAACTTATCATTAACACAATCCAAATTTGTGGCAATCTTTCTCACTGTGTTTTTCGCG	2160
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Qy	2281	AAAAAGAGTATTTTCTGTGATTAATCTTATGTAAATCTACCTGTGAGACATAGTCTGG	2340
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Qy	2401	GTACTTTCTTTAACCAGTATGAAATAAATGGCAAGTATCTATTCATGCTGTGGTAACA	2460
Db	2401	GTACTTTCTTTAACCAGTATGAAATAAATGGCAAGTATCTATTCATGCTGTGGTAACA	2460
Qy	2461	CCATCTCGATCCTGGTGTATGTACAAAATCTCTGGTGGGAAGCTGGTTATTTGGACA	2520
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Qy	2581	ACATCTCATATAGGGGTACAAAGGAAGAAAGCAGTAGTAATATACAAAAGTTTCTCTACT	2640
Db	2581	ACATCTCATATAGGGGTACAAAGGAAGAAAGCAGTAGTAATATACAAAAGTTTCTCTACT	2640
Qy	2641	GTTTGGGCAATATTTCCCTTCCAGTCTGTGTTTATAGCTAAGGAGCAGCATATTATTC	2700
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Db	2701	AGATTAATTTGTTACTGGCTTTAACAACATGAATTAAGCTTACTTTTCAATGCTTTATAATT	2760
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Best Local Similarity 100.0%; Pred. No. 0;
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Db	3121	ATGATTTGATTTGCCAATATACAGTTTTCCTAGTACTACAAACAAAGCTGTTCATGAAAC	3180
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Db	3181	ACCACTGATGCTAGATCATCGGAGACAATATGCGTATTCGCTAGCTTAAGACTTCACAT	3240
QY	3241	ATCCGCTCTTGGTTGCAGTTGGCAATATATACATTCCTGTTGCAGGAATTCGTGCATTTAC	3300
Db	3241	ATCCGCTCTTGGTTGCAGTTGGCAATATATACATTCCTGTTGCAGGAATTCGTGCATTTAC	3300
QY	3301	ATAAATCTATGCTGTGATTAACAAAGGCAAGAGTTGAGGAGACAACGGGAAATGTTTG	3360
Db	3301	ATAAATCTATGCTGTGATTAACAAAGGCAAGAGTTGAGGAGACAACGGGAAATGTTTG	3360
QY	3361	GTTTGGGGAAGAGCCGCTAAAGGTGTGATCTAATATAGCCCAACAACTAGCTGTGTGAC	3420
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Db	3421	TTAGCTATATATCCCTTTACACACCTAAACATTTTGAATGTATGAATCTCTTGGTCTCT	3480
QY	3481	CGGTTTGTTCAGATTTGTGGCGTGTATACACATCTGCTGAACCTAAACACTAGCTCT	3540
Db	3481	CGGTTTGTTCAGATTTGTGGCGTGTATACACATCTGCTGAACCTAAACACTAGCTCT	3540
QY	3541	TCTCTTAAACGCTGGAAGGAGAGATATCTCATATATCACTTCAACACCTAAACAAATAG	3600
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Db	4081	TATTACGTTAAATTCGAACGTTGGAAATCATCAAAAGACGTGCCAAACAAAAATGCAAT	4140
QY	4140	TGATGCGATAGACACTTTTTCGTGATTTGTATGCTATATAGTTTTCAAATCTTACGTAC	4199
Db	4141	TGATGCGATAGACACTTTTTCGTGATTTGTATGCTATATAGTTTTCAAATCTTACGTAC	4200
QY	4200	GCTTATGATTTCCCTAGATTATCAAAAGTTAGCTGCGCTTCTTCAATTTATTTATTTGA	4259
Db	4201	GCTTATGATTTCCCTAGATTATCAAAAGTTAGCTGCGCTTCTTCAATTTATTTATTTGA	4260
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Db	4321	ACTACATCAATTAAGTCTTTTATTAAGTACAGGCACTAATTAAGCTTGAACCTTAATAAA	4380
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Db	4501	AACTACTATTAACAGTTTTCACAAAATTTGATTCCTTATTTTATTTTCTTTGTCTCA	4560
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RESULT 3

US-09-817-774-32
: Sequence 32, Application US/09817774
: Patent No. US2002012011A1
: GENERAL INFORMATION:
: APPLICANT: CHOE, Sung-hwa
: APPLICANT: FELDMANN A., Kenneth
: TITLE OF INVENTION: D+FS MUTANTS
: FILE REFERENCE: 2225-0020 / 91020_002
: CURRENT APPLICATION NUMBER: US/09/817,774/4
: CURRENT FILING DATE: 2001-03-26
: PRIOR APPLICATION NUMBER: 60/192,202
: PRIOR FILING DATE: 2000-03-27
: NUMBER OF SEQ ID NOS: 45
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO: 32

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? ORGANISM: Arabidopsis thaliana
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? LOCATION: (3284)..(3304)
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[illegible]

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OY	121	ATTGCATCTCTTAACAATACATAAATTTTCGGAATAATGAAAAAAACTGAAAACCCANA	180
Db	121	ATTGCATCTCTTAAACAATACATAAATTTTCGGAATAATGAAAAAAACTGAAAACCCANA	180
OY	181	GAAITTCACACAGCATCAGAANAATAGATCTTAGGTTTTGCCGGGAGTTACCAAACAAATT	240
Db	181	GAAITTCACACAGCATCAGAANAATAGATCTTAGGTTTTGCCGGGAGTTACCAAACAAATT	240
OY	241	AGAAAAATGCATCTTACACAGAAATTCACCAATCTCGGAGATTTTCTTCCAAGCAAG	300
Db	241	AGAAAAATGCATCTTACACAGAAATTCACCAATCTCGGAGATTTTCTTCCAAGCAAG	300
OY	301	CCATTCGCTTGGAGATAGAAAGAAATTTGTAACATATGACAGCGCAATCACAGTAAGAGAA	360
Db	301	CCATTCGCTTGGAGATAGAAAGAAATTTGTAACATATGACAGCGCAATCACAGTAAGAGAA	360
OY	361	TTTGATTTTGTTAAGTCTCGATTCATCACTATGTTGTAATACAGAGATGACGAAGATCTT	420
Db	361	TTTGATTTTGTTAAGTCTCGATTCATCACTATGTTGTAATACAGAGATGACGAAGATCTT	420
OY	421	TTTGAGGTTTGAGAGAAGAAAGAGCTAAGAAATTTGGATCATCTAATAAACGATGGCAAGA	480
Db	421	TTTGAGGTTTGAGAGAAGAAAGAGCTAAGAAATTTGGATCATCTAATAAACGATGGCAAGA	480
OY	481	AAAGCTCAACAGGTAAATTTGGAATTTGAAAAAACAATGGAGAGACAGTGCACAGTGGG	540
Db	481	AAAGCTCAACAGGTAAATTTGGAATTTGAAAAAACAATGGAGAGACAGTGCACAGTGGG	540
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Db	541	AATTAATCTGAGTTTCACAGTAGACCTGTGAAAGTTCACTCGTTCATCGTTAACTTCGAG	600
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Db	601	ACTCGTTGATTATCAACAACAATCTAGATCTTGAGAGCTTTGGCCGAGACGAGAAAGCA	660
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Db	661	GAAAGAGAAATGGCGGAGACCTGACATCTTCGAGATCGTTACTAGCATGATGTATTC	720
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Db	721	GCTTCTCGCCTTCTGTCCACCTTTCGTGATCTTCCTGTAAAGTCATTAATTTCTGATTCG	780
OY	781	CAACTCTTATTCTAGTTCTCAGATCAAGCTCGCACACTTTTCTGCTCCTTAATTCATA	840
Db	781	CAACTCTTATTCTAGTTCTCAGATCAAGCTCGCACACTTTTCTGCTCCTTAATTCATA	840
OY	841	GCGAGAGTGCATGCGCGATATCTTTPAATCCCTTCCCANTTAAGTAGAGCTGATAAAG	900
Db	841	GCGAGAGTGCATGCGCGATATCTTTPAATCCCTTCCCANTTAAGTAGAGCTGATAAAG	900
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OY	1021	TCACAAGTTTCATTTCTTTAGATGCAAGATGATGATGCAATGATGATGATGATGATGATG	1080
Db	1021	TCACAAGTTTCATTTCTTTAGATGCAAGATGATGATGCAATGATGATGATGATGATGATG	1080
OY	1081	TTACTCAGACCTTTGCGTTCTTTTGGAGAAATGAGATTTAAGAGCTTATCAACAATATGCG	1140
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OY	1141	CAGAACCACCTTTCATGTTGTTGGAATAATATATTTTGTATGAGAGCAATTTGACATATTC	1200

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 Db 1201 TTCAGTGGCTTCTGCTGGTAAAGAGTTGAGGTCCTATCTCCAGCGGAACCCAGC 1260
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 Db 2101 CCAACTATCATATACACAATCAATTTGGGCAATCTTTTCACTGCTGTTTTCGGG 2160
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Db	4861	ATCTAAAAACAATTTTACTG 4880	

RESULT 4

US-09-817-774-34

Sequence 34, Application US/09817774

Patent No. US2002012011A1

GENERAL INFORMATION:

APPLICANT: CHOE, Sunghwa

APPLICANT: FELDMANN A., Kenneth

TITLE OF INVENTION: Dwf5 MUTANTS

FILE REFERENCE: 2225-0020 / 91020.002

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PRIOR APPLICATION NUMBER: 60/1192,202

PRIOR FILING DATE: 2000-03-27

NUMBER OF SEQ ID NOS: 45

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 34

LENGTH: 4880

TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: CDS

LOCATION: (671)..(757)

OTHER INFORMATION: dwf5-2

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LOCATION: (1050)..(1271)

OTHER INFORMATION: dwf5-2

NAME/KEY: CDS

LOCATION: (1340)..(1396)

OTHER INFORMATION: dwf5-2

NAME/KEY: CDS

LOCATION: (1505)..(1606)

OTHER INFORMATION: dwf5-2

NAME/KEY: CDS

LOCATION: (1711)..(1776)

OTHER INFORMATION: dwf5-2

NAME/KEY: CDS

LOCATION: (2174)..(2287)

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LOCATION: (2418)..(2546)

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 LOCATION: (2776)..(2874)
 OTHER INFORMATION: dwf5-2
 NAME/KEY: CDS
 LOCATION: (3321)..(3386)
 OTHER INFORMATION: dwf5-2
 NAME/KEY: CDS
 LOCATION: (3496)..(3525)
 OTHER INFORMATION: dwf5-2
 US-09-817-774-34

Query Match 99.7%; Score 4866.4; DB 10; Length 4880;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4878; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 DB 61 ATGTGATTCGTCGATAAATCTGCTTCCTTCATCATCATCATCATAGGACCTA 120
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 DB 121 ATTCGATCTCTAAACATCTAAATTTCTGGAATGAAAAAACTGGAAGCAAAA 180
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 DB 181 GAATTCACACACAGCATCAGAAAACTAGATCTAGTTTCCGGGAGTTACCAAAACATT 240
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 DB 1621 CATGATGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1680
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Oy 3061 AACAGACGGGAGAGAGATTAAGTGTATGATTAATGCTGCTGCTGCTGCTGCTGCTG 3120
Db 3061 AACAGACGGGAGAGATTAAGTGTATGATTAATGCTGCTGCTGCTGCTGCTGCTGCTG 3120
Oy 3121 ATGATTTGATTTGCTAGATATGATTTTCTAGTATGAGAAAGAGTGTATGAGAAAG 3180
Db 3121 ATGATTTGATTTGCTAGATATGATTTTCTAGTATGAGAAAGAGTGTATGAGAAAG 3180
Oy 3181 ACCACTGATGCTAGATATGCTGAGGACAAATATGCTGCTGCTGCTGCTGCTGCTGCT 3240
Db 3181 ACCACTGATGCTAGATATGCTGAGGACAAATATGCTGCTGCTGCTGCTGCTGCTGCT 3240
Oy 3241 ATCCGCTTTGCTGAGTGTGCAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Db 3241 ATCCGCTTTGCTGAGTGTGCAATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 3300
Oy 3301 ATAAATATGATGCTGATATGAGCAAAAGGCAAGTTCAGAGAGCAAAAGGCAAAATGTTG 3360
Db 3301 ATAAATATGATGCTGATATGAGCAAAAGGCAAGTTCAGAGAGCAAAAGGCAAAATGTTG 3360
Oy 3361 GTTTGGGAGAGAGCCCGTCAAAAGTGTATATTAAGCCCAATGCTTGTAGTGAAC 3420
Db 3361 GTTTGGGAGAGAGCCCGTCAAAAGTGTATATTAAGCCCAATGCTTGTAGTGAAC 3420
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Db 3421 TTAGCTATATTCCTTTGAGACCTTAACATTTTGTATGATATGCTTCTGCTGCTGCT 3480
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Db 3601 ACCTTTTCAATCAATGCTTTGAATGAGAGTGGGATTTGGCTGCTCAATTTCCAT 3660
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Db 3661 ATGTTCTGATCTTAAGTGTCTTCTGAGCCGTACCGGCTCTCTCGATTAACGTAA 3720
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Db 3721 AATAGTATCCATCTATTTGCTATTTGAGAGCTCTTCTGCAAGTAAAGCACTTAACA 3780
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Db 3781 TATAATCATCTTTGTTTAAACAGTTCCTTGGCATCTTCTACGTCATATTTCTACCT 3840
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Db 3841 TCTTCTTCTGATGAGCCAAAGAGAGAGATGACCGATGCCGATCAAGTAAAGCAACAA 3900
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Db 3961 GCTTTTGTGTTGTTAAAGGATGAGAAATTTGGAAGCTGATTTGAG- AAGTCAAA 4020
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Db 4021 TACAGATCATCTCCGGAAATTTATGATTTGAAGAGTCTGTTGCTCAATTTCTACT 4080
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Db 4261 TATTATGATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4320
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QY 4860 ATCTAAACAACTTTACTG 4879
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Db 4861 ATCTAAACAACTTTACTG 4880

RESULT 6

US-09-817-774-38
Sequence 38, Application US/09817774
Patent No. US2002012011A1
GENERAL INFORMATION:
APPLICANT: CHOE, Sunghwa
APPLICANT: FELDMANN A., Kenneth
TITLE OF INVENTION: DWFS MUTANTS
FILE REFERENCE: 2225-0020 / 91020_002
CURRENT APPLICATION NUMBER: US/09/817,774
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: 60/192,202
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 38
LENGTH: 4880
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: CDS
LOCATION: (671)..(757)
OTHER INFORMATION: dwfs-4
NAME/KEY: CDS
LOCATION: (1050)..(1271)
OTHER INFORMATION: dwfs-4
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OTHER INFORMATION: dwfs-4
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LOCATION: (1505)..(1606)
OTHER INFORMATION: dwfs-4
NAME/KEY: CDS
LOCATION: (1711)..(1776)
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LOCATION: (2174)..(2287)
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LOCATION: (3494)..(3559)
OTHER INFORMATION: dwfs-4
NAME/KEY: CDS
LOCATION: (3636)..(3716)
OTHER INFORMATION: dwfs-4
NAME/KEY: CDS
LOCATION: (3806)..(3889)
OTHER INFORMATION: dwfs-4
NAME/KEY: CDS
LOCATION: (3982)..(4047)
OTHER INFORMATION: dwfs-4
US-09-817-774-38

Query Match 99.7%; Score 4866.4; DB 10; Length 4880;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4878; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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Db 1 AACTGTCCTTCTCCACACAGATCTCTTTCCGGCTGCTAGATTTCTTTAAG 60
QY 61 ATGTGATTCGTCGAATAAATCTGCTTCTCTATCATCATCATCTAGGACCTA 120
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Db 61 ATGTGATTCGTCGAATAAATCTGCTTCTCTATCATCATCATCTAGGACCTA 120
QY 121 ATGTGATTCGTCGAATAAATCTGCTTCTCTATCATCATCATCTAGGACCTA 180
|||||
Db 121 ATGTGATTCGTCGAATAAATCTGCTTCTCTATCATCATCATCTAGGACCTA 180
QY 181 GAATTCACACAGCATCAGAAAACTAGATCTAGGTTCCCGGAGTTACCAAAACATT 240
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Db 181 GAATTCACACAGCATCAGAAAACTAGATCTAGGTTCCCGGAGTTACCAAAACATT 240
QY 241 AGAAAAATCGATCTTACACGAATTCACCAATTCGTGAGAAATTTCTCCAGGCAAG 300
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Db 241 AGAAAAATCGATCTTACACGAATTCACCAATTCGTGAGAAATTTCTCCAGGCAAG 300
QY 301 CCATTGCTTGGCGATGAAGAAATTGTTAACTATGACTGGCAATCGAGTGAAGAGA 360
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Db 301 CCATTGCTTGGCGATGAAGAAATTGTTAACTATGACTGGCAATCGAGTGAAGAGA 360
QY 361 TTGATTTTGTAGTCTGATTCATCATCTATGTGTAATACAGATGACGAATCTT 420
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Db 361 TTGATTTTGTAGTCTGATTCATCATCTATGTGTAATACAGATGACGAATCTT 420
QY 421 TTGAGGTTGAGAGAGAGAAAGCTAAGAAATTTGGATCATCAAAACGATGGCAAGA 480
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Db 421 TTGAGGTTGAGAGAGAGAAAGCTAAGAAATTTGGATCATCAAAACGATGGCAAGA 480
QY 481 AAAGTCTCAAGGTTAAATTTGGAATTAAGAAAAATGTGGAGACAGTGACAGTGG 540
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Db 661 GAAGAAGAAATGGCGAGACGTGATCTCCGATTCGTTACTTCCGATGATGTTATC 720
QY 721 GCTTCTCGCCTTCTGTCCACCTTTCGTCAATCTCTGTAAGCTCATCAATTTCTGATTG 780
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Db 721 GCTTCTCGCCTTCTGTCCACCTTTCGTCAATCTCTGTAAGCTCATCAATTTCTGATTG 780
QY 781 CAAGTCTTATTCTAGTTCTCGATCAGACTGCGACACTTTTCTGGCTTTAATTCATA 840
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Db 781 CAAGTCTTATTCTAGTTCTCGATCAGACTGCGACACTTTTCTGGCTTTAATTCATA 840
QY 841 GCGAGAGTGCATACCGCATATCTTAAATCTTCCCATTAAGTAGACTGATTAAG 900
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Db 841 GCGAGAGTGCATACCGCATATCTTAAATCTTCCCATTAAGTAGACTGATTAAG 900
QY 901 GCGAGAGTGCATACCGCATATCTTAAATCTTCCCATTAAGTAGACTGATTAAG 960
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Db 901 GCGAGAGTGCATACCGCATATCTTAAATCTTCCCATTAAGTAGACTGATTAAG 960
QY 961 TCTTTAATTTGAAAAAGCGATTCAATGATTTCTGTGGCAATGTGAATTTCCAGATT 1020
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QY 1021 TCACAGATTTCATTTCTTATGATGACAGATGTTACACATGTTATCAGATGTTCTG 1080
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Db 1021 TCACAGATTTCATTTCTTATGATGACAGATGTTATCACATGTTATCAGATGTTCTG 1080
QY 1081 TTACTCAGACCTTTGGCTTTCTTTGGAGAAATGAGTTCAAGACTTATCAACATATGCG 1140
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Db 1081 TTACTCAGACCTTTGGCTTTCTTTGGAGAAATGAGTTCAAGACTTATCAACATATGCG 1140

QY 1141 CAAGACCACTTGGATGGCTGGAAATATATTTGCTATGAGACATTTGAAGCATTC 1200
 Db 1141 CAAGACCACTTGGATGGCTGGAAATATATTTGCTATGAGACATTTGAAGCATTC 1200
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 Db 1201 TTCAGCTGCTTCTGCTGGTAAAGAGTTGAGGGTCCAAATATCTCCAGCCGGAACCCGAC 1260
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 Db 1261 CAGTTTACAAGGATATGTTCAATTAAGTCTGTGGTGAAGTTGATGACGATGACAACTG 1320
 QY 1321 TAGGCTCTTTCTTTCAGAGCCCAATGCTGGCTGCTCTTCTTCTTGTACACTGCAACCTA 1380
 Db 1321 TAGGCTCTTTCTTTCAGAGCCCAATGCTGGCTGCTCTTCTTCTTGTACACTGCAACCTA 1380
 QY 1381 TCTTGGCTTGGTGGTAAAGAAATGTTCCGATGACTTGGTTGGTTAACTTATGTT 1440
 Db 1381 TCTTGGCTTGGTGGTAAAGAAATGTTCCGATGACTTGGTTGGTTAACTTATGTT 1440
 QY 1441 TACGTAATCTTAACCTGGATTAAGTGTGACCTATGTCAGTTAATTTCTGCGCTATT 1500
 Db 1441 TACGTAATCTTAACCTGGATTAAGTGTGACCTATGTCAGTTAATTTCTGCGCTATT 1500
 QY 1501 CAGGTTTGAATCTTCAACCCCTGCAATGCTATGATCACTTGGGTAATTTTTCGCGC 1560
 Db 1501 CAGGTTTGAATCTTCAACCCCTGCAATGCTATGATCACTTGGGTAATTTTTCGCGC 1560
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 Db 1561 ACTAATATTCGGAAGCTTCATATTTGTGTTGTGATCAATAAAGTAAGTGTCTATTG 1620
 QY 1621 CAGTAATGCTGTCTTCTTGTGTTGTGATCAATAAAGTAAGTGTCTATTG 1680
 Db 1621 CAGTAATGCTGTCTTCTTGTGTTGTGATCAATAAAGTAAGTGTCTATTG 1680
 QY 1681 TTTGCTAAACTTATTTTCTTGTGATCAAGGCTGTCACCTTCACTCAAGTACTCT 1740
 Db 1681 TTTGCTAAACTTATTTTCTTGTGATCAAGGCTGTCACCTTCACTCAAGTACTCT 1740
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 Db 1741 GGTTCATGCTGAACCTTAATTAATGACTTCTATTTGGGTAGATTATTTCTGCTGATCAGAT 1800
 QY 1801 CTGATTTCTTTTGAATGCTGTGTGGGATTTATTTGAGAACTGCGGCTTACTGCCA 1860
 Db 1801 CTGATTTCTTTTGAATGCTGTGTGGGATTTATTTGAGAACTGCGGCTTACTGCCA 1860
 QY 1861 TCTCTCATATATTTTCTTCTTGTGATCAAGGCTGTCACCTTCACTCAAGTACTCT 1920
 Db 1861 TCTCTCATATATTTTCTTCTTGTGATCAAGGCTGTCACCTTCACTCAAGTACTCT 1920
 QY 1921 TCCAAATTTAGTACCTGTAAGCGAAATGTTCTTACAGATATTTATCTTTTATGAT 1980
 Db 1921 TCCAAATTTAGTACCTGTAAGCGAAATGTTCTTACAGATATTTATCTTTTATGAT 1980
 QY 1981 TTTAGTACAGAAAGTGTGTGGTGAATGTCGTGGTGAAGGAAAGAAAGAAAGTA 2040
 Db 1981 TTTAGTACAGAAAGTGTGTGGTGAATGTCGTGGTGAAGGAAAGAAAGAAAGTA 2040
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 Db 2041 TGCAGTAGTATTAACAATATCAAGTATGAGTCTCTCTCAGCACTGACTCTTTTGGT 2100
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 Db 2101 CCAACTTATATTAACAATATCAAGTATGAGTCTCTCTCAGCACTGACTCTTTTGGT 2160
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 Db 2161 TCGGCTTTCAGGAGTGTGATGACCTGCAATTTGGTAAGAGCTTTGACATCAAGGT 2220

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 Db 2281 AAAACAGGATTTTCTGATTAATTTCTTATGTAATTAATTAATTAATTAATTAATTAAT 2340
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 Db 2341 TGGTTTCTTTAAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2400
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 Db 2941 TTAGATACCACTTTTATACGAAAAAACAAGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 3000
 QY 3001 CCAATTTCTAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
 Db 3001 CCAATTTCTAGGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3060
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 Db 3061 AACAGACGGAGAGAGTAAAGTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 3120
 QY 3121 ATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
 Db 3121 ATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3180
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 QY 3361 GTTGGGGAAGAGCCCGTCAAGGTGATCATTAATAGCCCACTAGCTTAAGTAAC 3420
 Db 3361 GTTGGGGAAGAGCCCGTCAAGGTGATCATTAATAGCCCACTAGCTTAAGTAAC 3420
 QY 3421 TTACCTATATTCCTTTTCAAGCACTTAACATTTTGTATGATGATCTCTGTCCT 3480
 Db 3421 TTACCTATATTCCTTTTCAAGCACTTAACATTTTGTATGATGATCTCTGTCCT 3480
 QY 3481 CGGTTTGTGAGATTTGTGGCTGTATPACTACAACATCTGGTGAACCTAAACTAGCT 3540
 Db 3481 CGGTTTGTGAGATTTGTGGCTGTATPACTACAACATCTGGTGAACCTAAACTAGCT 3540
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 Db 4141 TGATGATGATGATCTTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4200
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 Db 4321 ACTACATCAATGATGCTTTTAACTAGTACAGCACTAATTTGAACCTATATATAA 4380
 QY 4380 TACATGATTAATCAAAAGATTAAGTGTCTTCTGATTTTCAATCAAAAGAACTC 4439
 Db 4380 TACATGATTAATCAAAAGATTAAGTGTCTTCTGATTTTCAATCAAAAGAACTC 4439

Db 4381 TACATGATTAATCAAAAGATTAAGTGTCTTCTGATTTTCAATCAAAAGAACTC 4440
 QY 4440 ACCGATTAATCAAGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4499
 Db 4441 ACCGATTAATCAAGTGTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4500
 QY 4500 AACTTATTAACAGCTTTTCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4559
 Db 4501 AACTTATTAACAGCTTTTCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4560
 QY 4560 AACTTATTAACAGCTTTTCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4619
 Db 4561 AACTTATTAACAGCTTTTCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4620
 QY 4620 AGCTAGAGAGCAATGCTCAAAACAAAGATTAAGAGGGAGCTCAAGAGCTCAAC 4679
 Db 4621 AGCTAGAGAGCAATGCTCAAAACAAAGATTAAGAGGGAGCTCAAGAGCTCAAC 4680
 QY 4680 CGAGTAGAGCAATGCTCAAAACAAAGATTAAGAGGGAGCTCAAGAGCTCAAC 4739
 Db 4681 CGAGTAGAGCAATGCTCAAAACAAAGATTAAGAGGGAGCTCAAGAGCTCAAC 4740
 QY 4740 GTACCAAGCTCTTCAAGCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4799
 Db 4741 GTACCAAGCTCTTCAAGCAAAATTTGATTTGATTTGATTTGATTTGATTTGATTTG 4800
 QY 4800 AAGTTTTTAAATCAAAACAAAGATTAAGAGGGAGCTCAAGAGCTCAAC 4859
 Db 4801 AAGTTTTTAAATCAAAACAAAGATTAAGAGGGAGCTCAAGAGCTCAAC 4860
 QY 4860 ATCTAAACAAATTTTACTG 4879
 Db 4861 ATCTAAACAAATTTTACTG 4880

RESULT 7
 US-09-817-774-40
 ; Sequence 40, Application US/09817774
 ; Patent No. US2002012011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOE, Sung-hwa
 ; APPLICANT: FELDMANN A., Kenneth
 ; TITLE OF INVENTION: Dwf5 MUTANTS
 ; FILE REFERENCE: 2225-0020 / 91020_002
 ; CURRENT APPLICATION NUMBER: US/09/817,774
 ; PRIOR APPLICATION NUMBER: 2001-03-26
 ; PRIOR FILING DATE: 2000-03-27
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 40
 ; LENGTH: 4880
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (671)..(757)
 ; OTHER INFORMATION: dwf5-5
 ; NAME/KEY: CDS
 ; LOCATION: (1050)..(1271)
 ; OTHER INFORMATION: dwf5-5
 ; NAME/KEY: CDS
 ; LOCATION: (1340)..(1396)
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 ; LOCATION: (1505)..(1606)
 ; OTHER INFORMATION: dwf5-5
 ; NAME/KEY: CDS
 ; LOCATION: (1711)..(1776)
 ; OTHER INFORMATION: dwf5-5
 ; NAME/KEY: CDS
 ; LOCATION: (2174)..(2287)
 ; OTHER INFORMATION: dwf5-5

NAME/KEY: CDS
 LOCATION: (2418)..(2546)
 OTHER INFORMATION: dwf5-5
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 LOCATION: (2776)..(2874)
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 LOCATION: (3259)..(3384)
 OTHER INFORMATION: dwf5-5
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 OTHER INFORMATION: dwf5-5
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 LOCATION: (3636)..(3716)
 OTHER INFORMATION: dwf5-5
 NAME/KEY: CDS
 LOCATION: (3806)..(3883)
 OTHER INFORMATION: dwf5-5
 US-09-817-774-40

Query Match 99.7%; Score 4866.4; DB 10; Length 4880;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4878; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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 DB 1321 TACGCTTCTTCTTGGAGGCGCAATGCTGCTGCTTACTTGTGACACTAGCAACCTA 1380
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Db	4741	GTAACAAGCTCCTTCACCAAAATGTGATTCATGTGTTGGATATCATGAGATCTACTTC	4800
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RESULT 8
 US-09-817-774-42
 : Sequence 42, Application US/09817774
 : Patent No. US2009120111A1
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 : GENERAL INFORMATION:
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 : APPLICANT: CHO, Sung-hwa
 : APPLICANT: FELDMANN A., Kenneth
 : TITLE OF INVENTION: DWT5 MUTANTS
 : FILE REFERENCE: 2225-0020 / 91020.002
 : CURRENT APPLICATION NUMBER: US/09/817,774
 : CURRENT FILING DATE: 2001-03-26
 : PRIOR APPLICATION NUMBER: 60/192,202

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1 PRIOR FILING DATE: 2000-03-27
2 NUMBER OF SEQ. ID NOS: 45
3 SOFTWARE: PatentIn Ver. 2.0
4 SEQ. ID NO. 42
5 LENGTH: 4880
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7 TYPE: DNA
8 ORGANISM: Arabidopsis thaliana
9 FEATURE:
10 NAME/KEY: CDS
11 LOCATION: (671)..(757)
12 OTHER INFORMATION: dwf5-6
13 NAME/KEY: CDS
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43 NAME/KEY: CDS
44 LOCATION: (3806)..(3892)
45 OTHER INFORMATION: dwf5-6
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47 US-09-817-774-42

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Query Match	Similarity	99.7%	Score	4866.4	DB	10	Length	4880
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Db	1	AACGTGCTCCCTCCACACAACAGATCTCTTTCGGGCTGTACGATTTTCGTTTAAAG	60					
QY	61	ATGTTGATTTCGTGCAATAAATCTGTCTTCTATCATCATCATCATCAGTAGGCACTA	120					
Db	61	ATGTTGATTTCGTGCAATAAATCTGTCTTCTATCATCATCATCATCAGTAGGCACTA	120					
QY	121	ATTGGATGCTCTAAACAATCTATAAATTTCTGAAATGAAAAAAACCTGAGAAACCAAAA	180					
Db	121	ATTGCATCTCTTAAACATCTATAAATTTCTGAAATGAAAAAAACCTGAGAAACGCAAAA	180					
QY	181	GAAATTCACACACGATCAGAAAACTAGATCTAGGTTTCGCGCGGAGTTACCAAAAAACATT	240					
Db	181	GAAATTCACACACGATCAGAAAACTAGATCTAGGTTTCGCGCGGAGTTACCAAAAAACATT	240					
QY	241	AGAAAAAATTCGATCTTACACGAAATTCGAGAAATTTCTTCCAAAGGCAG	300					
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Db	301	CGATTGCTTCGAGTAAGAAATTTGGTAACTCTGATCTGGAATTCAGAGTGAAGAGA	360					

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Db	661	GAAAGAAAGAAATGGCCGAGACTGATACATTTCTCCGATCTTACTTACGCATGCATGTTATC	720
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Db	1201	TTACGCTGCTTCTGCTGTTAAAGATGGAGGTCCTCAATATCTCCAGCCGGAACCGAC	1260
QY	1261	CAGTTTCAAGGTTATGTTCAATTAATGCTGTGGTGGAGAGTTGATGAGATGACAAATCG	1320
Db	1261	CAGTTTCAAGGTTATGTTCAATTAATGCTGTGGTGGAGAGTTGATGAGATGACAAATCG	1320
QY	1321	TACGGTTCTTTCTTTCGAGGCCAATGATGCTGCTGCTTCACTTTGACACTAGCAACTTA	1380
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QY	1381	TCTTGGCTTTGGTGGTAAABAAATGTTTCCGATGACTTTGGTTTGGTTAAAGTATGTT	1440
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QY	1441	TACGATATCGTAAGCTTGATTAAGGTTGGCAACCCATGTCAGTTAAATTCGTGCGCTAT	1500
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Db	1741	GGTGATGSGGAACCCATTAATTAATGACTCTATTTGGGTGAGTTATTTGCTGATCAAT	1800
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Db	2101	CCAACTTATCTTAAACAACAAATTCGGAACCTTTTCTGCACTGTGTTTTCGCG	2160
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RESULT 9

US-09-938-842A-4796
 ; Sequence 4796, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kieps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 4796
 ; LENGTH: 543
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-4796

Query Match 11.1%; Score 541.4; DB 9; Length 543;
 Best Local Similarity 99.8%; Pred. No. 3,7e-112;
 Matches 542; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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US-09-938-842A-3847
 ; Sequence 3847, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kieps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 3847
 ; LENGTH: 2000
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-3847

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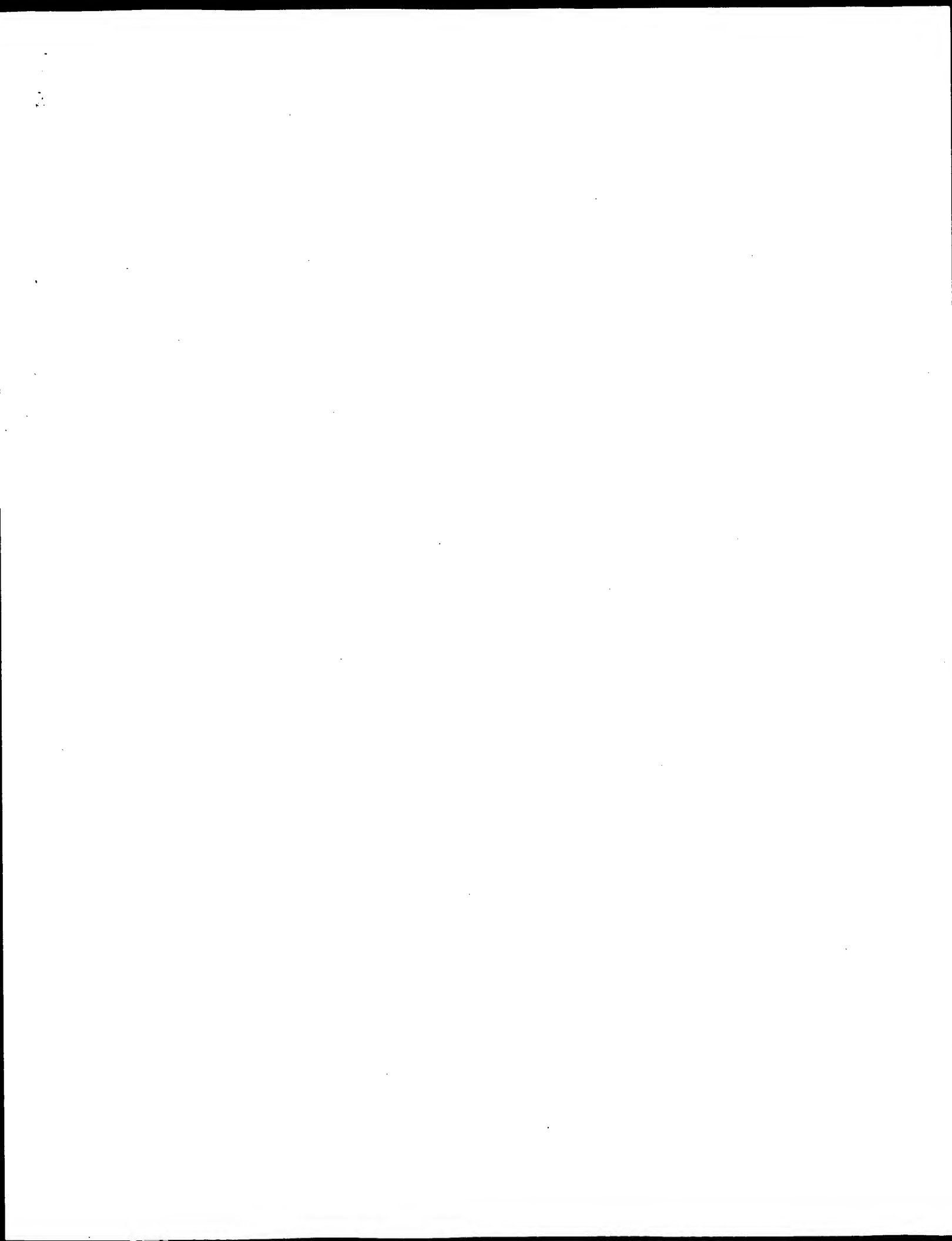
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RESULT 11

US-09-817-774-44
 ; Sequence 44, Application US/09817774
 ; Patent No. US2002012011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOE, Sung-hwa
 ; APPLICANT: FELDMANN A., Kenneth
 ; TITLE OF INVENTION: Dwf5 MUTANTS

Query Match	4.68;	Score 224;	DB 9;	Length 1299;
Best Local Similarity	100.08;	Pred. No. 8.2e-41;		
Matches 224;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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; Sequence 2109, Application US/09983965
; Patent No. US20020137160A1
; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Ningbing
; APPLICANT: Byatt, John C.



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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	237.4	4.9	1194	21 AAC36661	Arabidopsis thalia
4	224	4.6	1496	17 AAT93358	Arabidopsis thalia
5	87.8	1.8	354	21 AA69663	pinus radiata ster
6	79.2	1.6	629	21 AA66614	zebra mays DNA fragm
7	69.2	1.4	9539	22 AAS5347	Chemically pretrea
8	69.2	1.4	9539	24 AB528180	DNA transcription
9	68.8	1.4	6668	24 AB133697	Human immune syste

10	66.4	1.4	887	22 AAI94064	Human neuroblastom
11	64.2	1.3	34769	22 AAS46774	Tumour suppressor
12	63.8	1.3	6644	20 AAX33181	Base sequence of t
13	63.8	1.3	7372	20 AAX33182	Base sequence of t
14	63.8	1.3	7797	20 AAX33180	Cowpox virus bsr f
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KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
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PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
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KM protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
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Fri Jan 17 19:40:47 2003

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PF 25-FEB-2000; 2000EP-0301439.
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QY 61 ATGTGATGCTGGAATTAATCTGCTTCTATCATCATCATCATCATCATCATCAT 120
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QY 121 ATGCACTCTTAAACATTAATAATTTGGAATGAAATGAAATGAAATGAAATG 180
DB 235 ATGCACTCTTAAACATTAATAATTTGGAATGAAATGAAATGAAATGAAATG 191
QY 181 GAATTCACACACAGATCTAGATCTAGGTTCCCGGAGATGACCAAAACAT 240
DB 190 ----- 191
QY 241 AGAAAAATGATACCTTACACGATTCACCAATTTCTGGAGATTTCTTCCAAAGC 300
DB 190 ----- 150
QY 301 CCATGCTTCGAGTAGAAGAAATGTTAACTATGACTGCGAATCAGAGTGAAGAGA 360
DB 149 CCATGCTTCGAGTAGAAGAAATGTTAACTATGACTGCGAATCAGAGTGAAGAGA 90
QY 361 TTGATTTTGTAGTCTGATTCATCATATGTTGTAATACAGATGACGAAGATCT 420
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DB 89 TTGATTTTGTAGTCTGATTCATCATATGTTGTAATACAGATGACGAAGATCT 30
QY 421 TTGAGGCTTGAGAGAGAAAGCTAAGAA 449
DB 29 TTGAGGCTTGAGAGAGAAAGCTAAGAA 1

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RESULT 4
 AAT39358
 ID AAT39358 standard; cDNA; 1496 BP.

AC AAT39358;

DT 09-APR-1997 (first entry)

DE Arabidopsis thaliana delta-5,7-sterol, delta7-reductase cDNA.

KW Delta-7Red; 7-dehydrocholesterol reductase; C7-unsaturated sterol;

KW pregnenolone; plant; delta-5,7 sterol, delta-7 reductase;

KW nystatin resistance; ss.

OS Arabidopsis thaliana.

FT Key Location/Qualifiers

FT CDS 76..1368

FT /*tag= a

FT /EC_number= 1.3.1.21

PE 14-FEB-1996; 96EP-0400301.

PR 01-JUN-1995; 95FR-0006517.

PR 15-FEB-1995; 95FR-0001723.

PA (Rous) ROUSSEL-UCIAF.

PI Chenivresse X, Duport C, Lecain E, Pompon D;

DR WPI: 1996-372876/38.

DR P-PSDB: AAW03567.

PT Nucleic acid encoding delta-5,7 sterol delta-7 reductase - esp. of

PI A.thaliana, for producing pregnenolone-synthesising yeast.

PS Claim 3; Page 43-46; 82pp; French.

CC A nystatin-resistant clone containing cDNA which encodes the

CC delta-5,7 sterol, delta-7 reductase enzyme of Arabidopsis thaliana

CC was isolated from a cDNA library in yeast strain FY1679. The major

CC sterol of the untransformed yeast strain is ergosterol. RP-HPLC

CC analysis showed that in one clone the ergosterol was replaced by

CC two major sterols which did not absorb at 285 nm. The insert from

CC this clone was subcloned to localise the enzyme coding region and

CC the cDNA sequence was determined (i.e. the present sequence). The

CC enzyme, designated delta-7Red, reduces C7-unsaturated sterols. In

CC particular, it is useful in the production of pregnenolone.

Sequence 1496 BP; 399 A; 297 C; 340 G; 460 T; 0 other;

Query Match 4.6%; Score 224; DB 17; Length 1496;

Best Local Similarity 100.0%; Pred. No. 6.5e-42; Indels 0; Gaps 0;

Matches 224; Conservative 0; Mismatches 0;

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DB 162 ATGTAACAATGTTTCAATGATGTTCTTACTCAGACCTTTGGCTTTTGGGA 221
QY 1109 GAATGAGCTTCAAGACTTATCAACATATGCGCAAGACCACTTGTATGCTTGA 1168
DB 222 GAATGAGCTTCAAGACTTATCAACATATGCGCAAGACCACTTGTATGCTTGA 281

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Matches	99; Conservative	0; Mismatches	17; Indels	0; Gaps	0; Ns
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Db	118	GGGATATGGACCTTATTCCTCGAATAGCTAAACCTTTACATCAAGGCTTCAACAAATTG	177		
QY	2233	CAGATTCGAGATATGTTGGCAGTCTTGCAGTCTCAGTCACGTACGTAAACAG	2287		
Db	178	TCGGTTTGGAAATATATGCTTTGGCAGTCTTGCAGTAAACATACAGCATAAACAG	232		
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AAC46614					
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AC	AAC46614:				
XX					
DT	18-OCT-2000	(first entry)			
XX					
DE	Zea mays DNA fragment SEQ ID NO: 50785.				
XX					
KM	Hybridisation assay; genetic mapping; gene expression control;				
KM	protein identification; signal transduction pathway; metabolic;				
KM	pathway; promoter; termination sequence; corn; ss.				
XX					
OS	Zea mays subsp. mays.				
XX					
PN	EP1033405-AZ.				
XX					
PD	06-SEP-2000.				
XX					
PF	25-FEB-2000; 2000EP-030139.				
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PR	09-MAR-1999; 99US-0123548.				
PR	23-MAR-1999; 99US-0125788.				
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Search completed: January 16, 2003, 13:36:57
Job time : 1235 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 14:13:44 ; Search time 104 Seconds
(without alignments)
943.062 Million cell updates/sec

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Perfect score: 2594
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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2: SP_Archaea:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	553.5	21.3	620	11	008984
3	539.5	20.8	626	11	08VDM0
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5	518	20.0	418	6	08WV1
6	495	19.1	358	11	09CXP6
7	486.5	18.8	318	11	091227
8	435.5	16.8	249	11	091Y55
9	418.5	16.1	697	5	09XVF2
10	408	15.7	292	5	09GNP2
11	399	15.4	476	3	001461
12	397.5	15.3	399	11	091WJ6
13	351.5	13.6	441	5	09N751
14	350.5	13.5	622	3	09HEL3
15	272	10.5	67	10	0945E2
16	173.5	6.7	716	5	09W2D2

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18	119.5	4.6	284	10	09P865	09P865 oryza sativ
19	115.5	4.5	444	16	08XRK3	08XRK3 salmonella
20	112	4.3	791	10	08VXB2	08VXB2 oryza sativ
21	110.5	4.3	517	3	09HGM6	09HGM6 schizosacch
22	108.5	4.2	351	5	09U316	09U316 caenorhabdi
23	107.5	4.1	485	8	09G870	09G870 malawimonas
24	107	4.1	517	8	09B977	09B977 ceratocolen
25	106.5	4.1	524	8	09B972	09B972 ceratocolen
26	106.5	4.1	528	8	092800	092800 pyralidella
27	106.5	4.1	603	17	08TL61	08TL61 methanosarc
28	105.5	4.1	525	8	063228	063228 populus tre
29	105	4.0	499	16	08YMR6	08YMR6 anabaena sp
30	105	4.0	504	10	09SVR8	09SVR8 arabidopsis
31	105	4.0	750	8	095020	095020 tetrahymena
32	104.5	4.0	423	4	09H355	09H355 homo sapien
33	104.5	4.0	1027	5	0950C7	0950C7 caenorhabdi
34	104	4.0	571	8	09MLQ1	09MLQ1 limulus pol
35	103.5	4.0	471	8	09MH10	09MH10 buxus sp. g
36	103.5	4.0	569	8	09ARE8	09ARE8 lithobius f
37	103	4.0	471	5	09VT04	09VT04 drosophila
38	103	4.0	490	16	08XXR4	08XXR4 talstonia s
39	103	4.0	500	5	09VT03	09VT03 drosophila
40	102.5	4.0	76	3	09Y8E6	09Y8E6 neurospora
41	102.5	4.0	468	8	047441	047441 glinkgo billo
42	102.5	4.0	501	10	09FV14	09FV14 lotus japon
43	102.5	4.0	502	10	09FSH3	09FSH3 lotus japon
44	102	3.9	698	8	09SAR4	09SAR4 acrocomia a
45	101.5	3.9	462	2	051663	051663 paracoccus

ALIGNMENTS

RESULT 1
ID Q92228 PRELIMINARY; PRT; 471 AA.
AC 092228;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 7-DEHYDROCHOLESTEROL reductase (EC 1.3.1.21).
GN RD7R OR DHCR7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RA Nishino H., Ishibashi T.;
RT "Transmembrane configuration of sterol delta 7-reductase as a potential sterol sensing protein."
RL Submitted (Aug-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=SPRAGUE-DAWLEY;
RA MEDLINE=99262608; PubMed=10329655;
RA Bae S.-H., Lee J.N., Fletzky B., Seong J.K., Paik Y.-K.;
RT "Cholesterol biosynthesis from lanosterol. Molecular cloning, tissue distribution, expression, chromosomal localization, and regulation of rat 7-dehydrocholesterol reductase, a Smith-Lemli-Opitz syndrome-related protein."
RL T. Biol. Chem. 274:14624-14631(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Lee J.-N., Bae S.-H., Paik Y.-K.;
RT "Isolation and characterization of the rat 7-dehydrocholesterol reductase gene."
RL Submitted (Jun-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB018800; BAA34306.1;
DR EMBL; AF071500; AAD31383.1;
DR EMBL; AF279892; AAK69490.1; -

Query Match 20.8%; Score 539.5; DB 11; Length 626;
 Best Local Similarity 32.9%; Pred. No. 9.3e-41;
 Matches 135; Conservative 65; Mismatches 161; Indels 49; Gaps 12;

QY 18 ILAFPPVILLMTMWDGDSVOTFCFFENGVQGLINIPRTLIAMKIICGAF 77
 DB 251 LHFPPPLPAL-----HE-----LMEPRVCGYLLM-----VF-280

QY 78 AILQLLGKKEVEGIPSPAGNRPYKANGLAAYFYTLATYIGLMMFGIFNPAIYDHGE 137
 DB 281 ALFHLLPVGKAEGRPLVDGRRLQRLNGLAFILITSA-LGAAYFVGVELCYLYTHLQ 339

QY 138 IFSALIFGSPFYCVLLYIKGVADSSDS-GSCGNLIIDFYGMELPRICKSPDIKVT 196
 DB 340 LALATGFSVLLSAYLYVRSRLAPREELSPASSGNAVYDFIGRELNPRIQ-ANDLAFPC 398

QY 197 NCRGMMGAVLATYTCIKOYEINGKVSDSM-LVNTIIMLVYVTFEWMAGYNTMD 253
 DB 399 ELRPGELIGWVYINLMMLMEKKIQERAPSLAMITVNS-FQLLYVDALMNEELTLTSM 457

QY 254 IAHDRGFYICWGCLWVPSYVTSFGMYLVNHPYELGTOLAIYIIVAGILCIYINYDC-D 312
 DB 458 IMHGFEGMLAFGDLVWVPFTYSLOAFYLVSHPHDLSPILA-SYIILAKLCGYIFPCAN 516

QY 313 RQDBERRNGKCLVWGAPSKIVASYTTTSGETKSTLLTSGWGLARHHPYELISA 372
 DB 517 SOKNAFRKN-----PTDKALHKTHTSTGSKSLVSGWGWGRHBNYIGDLIMA 566

QY 373 FFWVVPALFDMFLAYFYIFLTLFPDRAKDDRCRSKYKYLKCEK 422
 DB 567 LAMSLPCGFHLLPYFYIYFTALLIHRDEHOCRRKYGLAWEKCYCOR 616

RESULT 4
 Q9W708 PRELIMINARY; PRT: 620 AA.

AC Q9W708;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Lamin B receptor.
 GN P58 GENE.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99323925; PubMed=10393814;
 RA Gajewski A., Krohne G.;
 RT "Subcellular distribution of the Xenopus p58/Lamin B receptor in oocytes and eggs";
 RL J. Cell Sci. 112:2583-2596(1999).
 DR EMBL: Y17842; CABA4317.1; -;
 DR Interpro: IPR000515; BPD_transp.
 DR Interpro: IPR001171; ERG4_ERG24.
 DR Interpro: IPR002999; Tudor.
 DR Pfam: PF01222; ERG4_ERG24; 1.
 DR SMART: SM00333; Tudor. 1.
 DR PROSITE: PS00402; BPD_TRANSF_INN_MEMBER; UNKNOWN_1.
 KM Receptor.
 SQ SEQUENCE 620 AA; 71128 MW; B70179E01F57C5EA CRC64;

Query Match 20.7%; Score 537.5; DB 13; Length 620;
 Best Local Similarity 31.0%; Pred. No. 1.4e-40;
 Matches 135; Conservative 71; Mismatches 177; Indels 53; Gaps 9;

QY 3 EYVHSPIVYASMSLIAF--CPEVILLMTMWDGDSV-----QTFGEWE 49
 DB 210 KNEENPKIAGGAIIGFLFMWCVP--ALTYLLLVCGOQYTSQGFVEILDIVGFGF-- 265

QY 50 NGVGLINIPRTLIAMKIIFCGAFEAIIQLLPGRKVEGPISPAGNRPYKANGLA 109

DB 266 -----VIMTL-----QVILLYLPGRKYVDGQNLKNGRLKTRISGCSA 304

QY 110 YEVTLATYIGLMMFGIFNPAIYDHLGEISALIFGSPFYCVLLYIKGVADSS--SDSG 167
 DB 305 FFLTAIMAGMKKKYVEINFLYIEHYLOFASATLSFSLISLYVRSYKVPNEELSMNA 364

QY 168 SCGNLIIDFYGMELPRICKSPDIKVTNCRGMMGAVLATYTCIKOYEIN-GKVD 225
 DB 365 NSGNFYIKFVWGRINERIG-NIDLVFVYVIRQALMSWVILINIMLAEKVKHMDPSL 423

QY 226 SMLVNTIIMLVYVTFEWMAGYNTMDIAHDGGEFYICWGCLWVPSYVTSFGMYLVN 285
 DB 424 SMLVNSFOLLVLDGFWNNEFYFLMSPDIYRDOFGFLAFGLSIAVAPFTYSLOTYLVN 483

QY 286 PVELGTOLAIYIIVAGILCIYINYDCRQREERRNGKCLVWGAPSKIVASYTTTSGE 345
 DB 484 PVDLSRQASAIVALFLGYIIRGANNOKCAFRON-----PDDPRLSHLKTPT 533

QY 346 TKTSLITSGWGLARHHPYELISAFWYVAPALDNFLAYFYIFLTLFPDRAKRD 405
 DB 534 SAGSKLITSGWGFVRHNPYLDIIMALAMCIACGPHLLPYFYIFLTLIDRAARDE 593

QY 406 DRCRSKYKYLKCE 421
 DB 594 QRCREKYGDMWKYQC 609

RESULT 5
 Q8WNV1 PRELIMINARY; PRT: 418 AA.

AC Q8WNV1;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE C-14 sterol reductase.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX PubMed=11784322;
 RA Roberti R., Bennati A.M., Galli G., Caruso D., Maras B., Alsa C.,
 RT "Cloning and expression of sterol Delta14-reductase from bovine liver";
 RL Eur. J. Biochem. 269:283-290(2002).
 DR EMBL: AY039681; AAK91505.1; -;
 DR Interpro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24; 1.
 DR PROSITE: PS01017; ERG4_ERG24_1; UNKNOWN_1.
 DR PROSITE: PS01018; ERG4_ERG24_2; UNKNOWN_1.
 SQ SEQUENCE 418 AA; 46751 MW; 30DE297CFE09568C CRC64;

Query Match 20.0%; Score 518; DB 6; Length 418;
 Best Local Similarity 35.3%; Pred. No. 5.4e-39;
 Matches 129; Conservative 57; Mismatches 153; Indels 26; Gaps 10;

QY 67 WKIIFC-YGAFEAIIQLLPGRKVEGPISPAGNRPYKANGLAAYFYTLATYIGLMMFG 124
 DB 61 WMLLCLLGMIGQALMYLIPARKVAEGGLKDKSLRKYPTNFQALVLT-ALLVGL---G 116

QY 125 INPAIYDHLGEISALIFG----SFIFCVLLYIKGVADSS--SDSGSCGNLIIDFY 178
 DB 117 V-SAGIPLSALPEMLPLPLFAATLTAFIFSLLYIKALAPASALAPGNSGNLIYDFL 175

QY 179 GMEIYPRICKSPDIKVTNCRGMMGAVLATYTCIKOYEINGKVSDSMLVNTIIMLVY 238
 DB 176 GRELNPRT-CSDFKFCFLRGLIGWVLIINALLIQEALIGSPSLMMLVNGFOLLIV 234

QY 239 TKFWMAGYNTMDIAHDGGEFYICWGCLWVPSYVTSFGMYLVNHPYELGTOLAIYIL 298

DB 235 GDAWTEBEAVLTITMDIHHGFGMLAFGLAWPFYTSIOAGFLYHPRLDMPPLASFIC 294
 QY 299 VAGILCIYINCDROQROEERTNGKCLWGRAP-S-KIVASTTSGERTKSLTSGMW 357
 DB 295 LINAAGYIFRGANSOKNFRKN-----PSDPRVADELTISTATGRRLTY-SGMW 343
 QY 358 GLARHFFHYVELLSAFWVVPALFDFNLAFYVIFLTLFPRARDDRCRSKYKWK 417
 DB 344 GMRVHPHYLGDLLMALWSLPCGVFHLPLPYFLYFTALLVHREDEROCROKYLAWH 403
 QY 418 LYCEK 422
 DB 404 EYCR 408

RESULT 6
 Q9CXP6 PRELIMINARY; PRT; 358 AA.

ID 09CXP6
 AC 09CXP6
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 GN 3110041018RIK protein.
 GN 3110041018RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
 RX MEDLINE=21085660; PubMed=11717851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glassi C., King B., Koehne H.,
 RA Kuehl P., Lewis S., Matsuo T., Nikaido I., Pesole G., Quackenbush J.,
 RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitlaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection."
 RL Nature 409:685-690(2001).
 DR EMBL: AK014166; BAB29187.1; -;
 DR MGD: MGI:1920416; 3110041018RIK.
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24_1; UNKNOWN_1.
 DR PROSITE: PS01017; ERG4_ERG24_1; UNKNOWN_1.
 DR PROSITE: PS01018; ERG4_ERG24_2; 1.
 SQ SEQUENCE 358 AA; 39719 MW; 0DD8D4AB2DE0275C CRC64;

Query Match 19.1%; Score 495; DB 11; Length 358;
 Best Local Similarity 34.6%; Pred. No. 5, 6e-17;
 Matches 113; Conservative 58; Mismatches 134; Indels 22; Gaps 8;

QY 102 YKANGLAAYVTATYGLMWFGEIFNPAIVYDHLGELISALIFG---SEIFCVLLYIKG 157
 DB 38 FVGFQALVLT-ALLMGL---GV-SVGLPLGALPGMLPLAFATITLTSFISLLIYAKA 92
 QY 158 HVAPSS--SSGSGGNLIDPYWGMELYPRIKGFIDKVTYNTNCRFGMSNAVALAVTYCIK 215
 DB 93 LVAPASALAGGNSGNSMDYDFLGRLELNPRIIG-SFDEKYPCELRPGILGWVFINALLMQ 151

QY 216 QYEINGKVSMDLNTILMLVYTKFFWMEAGYNNMDIAHRCGFYICWGCLVWVPSY 275
 DB 152 EAEELGSPSLAMMLVNGFOLLVYGDALMYEESVLTITMDIHHGFGMLVGDGLAWPFY 211
 QY 276 TSPGMVYNHPELGTOLAIVAGILCIYINCDROQROEERTNGKCLWGRAPSKI 335
 DB 212 SLAQFLYHPQPLGLPALLICLLKLVGYIFPGANSOKNFRKNPSDSVAG----- 265
 QY 336 VASTTSGERTKSLTSGMWGLARHFFHYVELLSAFWVVPALFDFNLAFYVIFLTL 395
 DB 266 LETIPTARGRQ---LVVSGMGVRRHPNYLGDLLMALWSLPCGLSHLLPYEVLVFTA 321
 QY 396 LLEPRARDDRCRSKYKWKLYCEK 422
 DB 322 LIVHREARDEOQCIQKGRAMQETCKR 348

RESULT 7
 Q91227 PRELIMINARY; PRT; 318 AA.

ID 091227
 AC 091227
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical 36.4 kDa protein (Fragment).
 GN A1505894.
 GN A1505894.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Strausberg R.;
 RA Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BC010261; AAH10261.1; -;
 DR MGD: MGI:2138281; A1505894.
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24_1; UNKNOWN_1.
 DR PROSITE: PS01017; ERG4_ERG24_1; UNKNOWN_1.
 DR PROSITE: PS01018; ERG4_ERG24_2; UNKNOWN_1.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 318 AA; 36384 MW; 91A05EB39274E398 CRC64;

Query Match 18.8%; Score 486.5; DB 11; Length 318;
 Best Local Similarity 34.5%; Pred. No. 2, 9e-36;
 Matches 111; Conservative 59; Mismatches 133; Indels 19; Gaps 8;

QY 106 GLAAVFTATYGLMWFGEIFNPAIVYDHLGELISALIFGFCVLLYIKGHVAPSSSD 165
 DB 1 GLVAFILTSAA-LGAAVFWGVELCYLTHFLOLALATGFSVLLSAYLVRSRLAPREEL 59
 QY 166 S-GSGCNLIDPYWGMELYPRIKGFIDKVTNCRFGMSNAVALAVTYCIQYEINIKVS 224
 DB 60 SPASGNAVYDFEIRLEINPRIG-AFDLKFCELRPGILGWVINLWLMEMTIOERAA 118
 QY 225 DSM--LVNTIIMLVYTKFFWMEAGYNNMDIAHRCGFYICWGCLVWVPSYTPGM 281
 DB 119 PELAMILVNS-FQLIYVDALMNEALLTSMIDIMHDSGFMALAGDLYWVFTYSLOAFY 177
 QY 282 LVNHPELGTOLAIVAGILCIYINCDROQROEERTNGKCLWGRAPSKIYASYT 340
 DB 178 LVSHPHDLSWPLA-SVITALKCGYVIFRANCSOKNARKN-----PTDPKLAHL 226
 QY 341 TTSGETKSLTSGMWGLARHFFHYVELLSAFWVVPALFDFNLAFYVIFLTLFDR 400
 DB 227 KTIHTSTGKSLVSGMWGEVRRHPNYLGDLLMALWSLPCGNHLLPYFYIIVFALLIHR 286
 QY 401 AKRDDRCRSKYKWKLYCEK 422
 DB 287 EARDEHQCRKRYIGLAMEYCKR 308

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RESULT 8
Q91YS5 ID 091YS5 PRELIMINARY; PRT; 249 AA.
AC 091YS5;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Hypothetical 29.0 kDa protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC014835; AAI14835.1;
DR InterPro: IPR001171; ERG4_ERG24.
DR Pfam: PF01222; ERG4_ERG24; 1.
DR PROSITE: PS01018; ERG4_ERG24_2; UNKNOWN_1.
KW Hypothetical protein.
FT NON_TER
SQ SEQUENCE 249 AA; 28955 MW; 86CF29C0E75341BF CRC64;

Query Match 16.8%; Score 435.5; DB 11; Length 249;
Best Local Similarity 35.7%; Pred. No. 1e-31;
Matches 90; Conservative 50; Mismatches 95; Indels 17; Gaps 6;

QY 175 DEFWGMELVTRICKSPDIKFTNCRFGMSMAVLAVTYCKQYEINGKVSDSM---LVNT 231
DB 1 DFFGRLANPLRG-APFLKFFCELRLPGLIGWVYINVLMLMEKIKDERAPSLAMILVNS 59
QY 232 ILMVLYTKFFWEGAGYWNMDIAHDRGFFYICGCLVWVPSYTSFGVLYVHNPVELGT 231
DB 60 -FGLLYVVDALWMEALALTSMIDIMHDSFGMLAFGLDLYWVPTYSQAFLVSHPHDLSW 118
QY 292 QLAIIYIVAGILCIYINDC-DROROEFRTNCKLVGRAPSKIYASVTTTSGETKTSL 350
DB 119 PLA-SVIAIKRLGCVYIFRCANSOKNAFRKN-----PDPKLAHLKTIHTSTGKS 167
QY 351 LITSGMGLARHPHYVEIISAFPMVPALEFDFLAVFYVIFLTLFLDARKDDDCRS 410
DB 168 LTVSGMGEFVRHPYVLDLIMALMSLPCGFINLLPEFYITFTALLIHRARDEHQCR 227
QY 411 KYGRYMKLYCEK 422
DB 228 KYGLAMEKCYOR 239

RESULT 9
Q9XVF2 ID 09XVF2 PRELIMINARY; PRT; 697 AA.
AC 09XVF2;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE B0250.9 protein.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Lloyd C.R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=9069613; PubMed=9851916;
RX none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology.";
RL Science 282:2012-2018(1998).

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DR EMBL: Z81453; CAB03797.1; -.
DR InterPro: IPR002106; AARNA_LigaseI.
DR InterPro: IPR002892; DUF40.
DR InterPro: IPR001171; ERG4_ERG24.
DR Pfam: PF01838; DUF40.1.
DR Pfam: PF01222; ERG4_ERG24; 1.
DR PROSITE: PS00339; AA-TRNA LIGASE II 2; UNKNOWN_1.
SQ SEQUENCE 697 AA; 79878 MW; 4B93C5E1A5D6C8 CRC64;

Query Match 16.1%; Score 418.5; DB 5; Length 697;
Best Local Similarity 29.3%; Pred. No. 1.2e-29;
Matches 122; Conservative 76; Mismatches 200; Indels 19; Gaps 9;

QY 10 VTYASMLSLACPPVILLMTWVHQC-----SYTGFGFWENGQGLIYNRPPLI 65
DB 286 VSAQWVALLIIVPAPTEFLFYISIHGLFVPTITAFLEP-PLVLCVPPVW---DTV 341
QY 66 AMKIFCYGAPFAILLQILLPGKRVESPISPAGNRPPYKANGLAAYFVLATYGLMFGI 125
DB 342 AMKFSVHCAIQILFVWVPHDQAL-VKSSAGDQ-MREVNSFSCILICLLVIGASAGV 399
QY 126 FNPALVYDHLGETFSALLFGSFIICVLLYIKGVAPSSSDSCGNLIIDFYMGELYPH 185
DB 400 YRGDLVYLHFNSEII-LIFA--IFAVLLW---AALIAHYHGVVTTISEFWGIENHPK 451
QY 186 ICKSPDIKFTNCRFGMSMAVLAVTYCKQYEINGKVSDSMVLNTIIMLYVTKFFWWE 245
DB 452 I-LDDIDLKFTIRTFEVLVPLFVLSAMVFKITVQISTSLVCLSSVQLLYIFQPHNE 510
QY 246 AGYWNMTDIAHDRGFFYICGCLVWVPSYTSFGVLYVHNPVELGTQAIYIVAGILCI 305
DB 511 DFLNSLDSKRCDFGYRIAMADFLVGLIITISPVILVATNSVVISNCLCAVALISM 570
QY 306 YINYDCDROROEFRTNCKLVGRAPSKIYASVTTTSGETKTSLLTSGMGLARHPHY 365
DB 571 VETACDRQKYEFRKRSKGLIKGVDAEFISAKYRTSDGADANTNLLSGHGVCRHPNY 630
QY 366 VPEIISAFPMVPALEFDFLAVFYVIFLTLFLDARKDDDCRSKYKMYKLYCEK 422
DB 631 ASEAITFAFSAFQGPFTIAHIPSLEFVILVAFRTDENCKLIKIQWMAQYCSK 687

RESULT 10
Q9GNE2 ID 09GNE2 PRELIMINARY; PRT; 292 AA.
AC 09GNE2;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE Putative sterol C-14 reductase (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RA Bhavani T.P.; Kasbekar D.P.;
RT "Genomic sequence of the putative sterol C-14 reductase of
RT Dictyostelium discoideum.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Prakash A.; Prasanna B.T.; Kasbekar D.P.;
RT "SSG792 cDNA encoding the putative sterol C-14 reductase of
RT Dictyostelium discoideum.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF308471; AAG30272.1; -.
DR EMBL: AF308470; AAG30271.1; -.
DR InterPro: IPR001171; ERG4_ERG24.
DR Pfam: PF01222; ERG4_ERG24; 1.
DR PROSITE: PS01017; ERG4_ERG24_1; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 292 AA; 34205 MW; 4A7F42DA72F1C53E CRC64;

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RESULT 14			
09HEL3			
ID	09HEL3	PRELIMINARY;	PRT; 622 AA.
AC	09HEL3;		
DT	01-MAR-2001 (TRENBLREL, 16, Created)		
DT	01-DEC-2001 (TRENBLREL, 19, Last sequence update)		
DE	01-MAR-2002 (TRENBLREL, 20, Last annotation update)		
GN	Probable sterol C-24 reductase.		
OS	12F11.140.		
OC	Neurospora crassa.		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;		
OC	Sordariales; Sordariaceae; Neurospora.		
OX	NCBI_TaxID=5141;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Schulte U., Aign V., Hohensei J., Brandt P., Fartmann B., Holland R.,		
RA	Myakutana G., Mewes H.W., Mannhaupt G.;		
RL	submitted (Dec-2000) to the EMBL/GenBank/DBJ databases.		
RL	[2]		
RP	SEQUENCE FROM N.A.		
RA	German Neurospora genome project;		
RA	Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.		

Dy 368 ELSAFTWTPALDENFLAIRVIFLTLLFDRAKRODDRCRSYGYGKYWLCEK 422
:
Dd 3 QILSAFTWTPALENHFLPFEEVIFLTLLFDRAKRODDRCRSYGYGKYWKPCCK 57

Fri Jan 17 19:40:59 2003

us-09-817-774-31.rsp

Job time : 108 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 14:13:05 ; Search time 13 Seconds

(Without alignments)
1518.672 Million cell updates/sec

Title: US-09-817-774-31

Perfect score: 2594

Sequence: 1 MAETVHSPIVTVASMLSLA.....RAKTKMQIDAIDILLICML 476

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2312	89.1	432	1	ST7R_ARATH
2	710.5	27.4	471	1	DHC7_MOUSE
3	698.5	26.9	475	1	DHC7_HUMAN
4	554	21.4	637	1	LBR_CHICK
5	544	21.0	615	1	LBR_HUMAN
6	503.5	19.4	430	1	ER24_ASCIM
7	500.5	19.3	424	1	ER24_SCHPO
8	499.5	19.3	418	1	ER24_HUMAN
9	473.5	18.3	490	1	ER24_NEUCR
10	470.5	18.1	369	1	ER24_ARATH
11	459.5	17.7	485	1	ER24_FUSSO
12	458.5	17.7	512	1	ER24_SEPLY
13	424.5	16.4	438	1	ER24_YEAST
14	371	14.3	473	1	ER24_YEAST
15	364.5	14.1	453	1	ST3_SCHPO
16	121	4.7	460	1	AT13_LYCES
17	120.5	4.6	524	1	COX1_BETVU
18	115.5	4.5	527	1	COX1_ARATH
19	108	4.2	599	1	THIV_YEAST
20	106	4.1	354	1	OPSD_YEAST
21	106	4.1	474	1	OPSD_CARAU
22	105	4.0	504	1	NU4M_PARTE
23	104.5	4.0	1418	1	AT14_ARATH
24	104	4.0	632	1	CE11_CAEEL
25	104	4.0	444	1	NU4M_LOCM1
26	102	3.9	438	1	AFUB_HAEIN
27	101.5	3.9	514	1	SECV_MERYA
28	101.5	3.9	522	1	AT12_LYCES
29	101.5	3.9	522	1	COX1_MAPPO
30	101	3.9	598	1	THIV_YEAST
31	100.5	3.9	354	1	OPSD_POBRE
32	100	3.9	485	1	YJDL_ECOLI
33	98.5	3.8	558	1	OPSD_CYPCA
					CX1B_PARDE

34	97.5	3.8	173	1	NU6M_LATCH	003175 latimeria c
35	96.5	3.7	524	1	COX1_ORYSA	P14578 oryza sativ
36	96.5	3.7	528	1	COX1_MAIZE	P08742 zea mays (m
37	96.5	3.7	530	1	COX1_SORBI	P05502 sorghum bic
38	96	3.7	354	1	OPSD_SALPY	Q94923 salaripa pav
39	96	3.7	459	1	YRPL_YEAST	P53584 saccharomyc
40	95.5	3.7	389	1	LGT_MYCPN	P75547 mycoplasma
41	95.5	3.7	524	1	COX1_WHEAT	P08741 triticum ae
42	95	3.7	514	1	AT12_ARATH	Q92PJ8 arabidopsis
43	94	3.6	687	1	AFUB_ACTPL	Q44123 actinobacil
44	94	3.6	702	1	NU5C_POAPR	Q32880 poa pratens
45	93	3.6	354	1	OPSD_ORYLA	P87369 oryzias lat

ALIGNMENTS

RESULT 1
ST7R_ARATH STANDARD: PRT: 432 AA.
ID ST7R_ARATH
AC 09LDT6; Q38930; (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 7-dehydrocholesterol reductase (EC 1.3.1.21) (7-DHC reductase) (Sterol
delta-7-reductase) (Dwaf5 protein).
GN DW5 OR ST7R OR AT1G50430 OR F11F12.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC TISSUE-Seeding;
RX MEDLINE=96210024; PubMed=8631902;
RA Lecain E., Chenivesse X., Spagnoli R., Pompon D.;
RT "Cloning by metabolic interference in yeast and enzymatic
characterization of Arabidopsis thaliana sterol delta 7-reductase.";
RL J. Biol. Chem. 271:10866-10873(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. WS-2;
RX MEDLINE=20223137; PubMed=10758495;
RA Choe S., Tanaka A., Noguchi T., Fujioaka S., Takatsuto S., Ross A.S.,
RA Tax F.E., Yoshida S., Feldmann K.A.;
RT "Lesions in the sterol delta reductase gene of Arabidopsis cause
dwarfism due to a block in brassinosteroid biosynthesis.";
RL Plant J. 21:431-443(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. Columbia;
RX MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremenetskaia I., Kutz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malti R., Marzilli A.,
RA Miltischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uteback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
thaliana.";
RL Nature 408:816-820(2000).
CC -I- FUNCTION: Production of cholesterol by reduction of C7-C8 double

CC bond of 7-dehydrocholesterol (7-DHC). Lesions in the gene coding
 CC for the enzyme cause dwarfism.
 CC -1- CATALYTIC ACTIVITY: Cholesterol + NADP(+) = cholesta-5,7-dien-3-
 CC beta-ol + NADPH.
 CC -1- PATHWAY: Sterol biosynthesis. Also participate in brassinosteroid
 CC (BR) biosynthetic pathway.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum.
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
 CC -----
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 CC -----
 DR EMBL: U49398; AAC49278.1; -;
 DR EMBL: AF239701; AAF63498.1; -;
 DR EMBL: AC012561; AAF87888.1; -;
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24; 1.
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 KW Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane;
 KM Endoplasmic reticulum.
 FT TRANSMEM 12 34 POTENTIAL.
 FT TRANSMEM 64 86 POTENTIAL.
 FT TRANSMEM 107 126 POTENTIAL.
 FT TRANSMEM 136 155 POTENTIAL.
 FT TRANSMEM 195 212 POTENTIAL.
 FT TRANSMEM 227 249 POTENTIAL.
 FT TRANSMEM 261 283 POTENTIAL.
 FT TRANSMEM 287 309 POTENTIAL.
 FT TRANSMEM 371 393 POTENTIAL.
 FT TRANSMEM 257 257 D -> N (IN DMF5-4; DWARF PLANT).
 FT VARIANT 257 257 Y -> H (IN REF. 1).
 FT CONFLICT 117 117 N -> K (IN REF. 1).
 FT CONFLICT 308 308
 FT CONFLICT 391 392 MISSING (IN REF. 1).
 SQ SEQUENCE 432 AA; 49591 MW; 5458E495BE1E4B0 CRC64;

Query Match 89.1%; Score 2312; DB 1; Length 432;
 Best Local Similarity 99.8%; Pred. No. 7.1e-163;
 Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAETVSPITVYASMLSLAFCEPPIVLLMYWHDGCVTQTFGFWEVNGVGLINIMP 60
 DB 1 MAETVSPITVYASMLSLAFCEPPIVLLMYWHDGCVTQTFGFWEVNGVGLINIMP 60

QY 61 RPLLIAMKIFFCYGAFFAIIQLLLPKRVEGPISPAGNRPVYKANGLAAYFTLATYGL 120
 DB 61 RPLLIAMKIFFCYGAFFAIIQLLLPKRVEGPISPAGNRPVYKANGLAAYFTLATYGL 120

QY 121 WMFGIFNPAIVYDHLGEISFALIFGSEIFCVLLYKINGHVAAPSSDSCGNLIIDFYWGM 180
 DB 121 WMFGIFNPAIVYDHLGEISFALIFGSEIFCVLLYKINGHVAAPSSDSCGNLIIDFYWGM 180

QY 121 WMFGIFNPAIVYDHLGEISFALIFGSEIFCVLLYKINGHVAAPSSDSCGNLIIDFYWGM 180
 DB 121 WMFGIFNPAIVYDHLGEISFALIFGSEIFCVLLYKINGHVAAPSSDSCGNLIIDFYWGM 180

QY 181 ELXPRIGKSDIVFTNCRGMMKSAVLAITYCIKOYEINGKYSDDLVTIMLYYTKR 240
 DB 181 ELXPRIGKSDIVFTNCRGMMKSAVLAITYCIKOYEINGKYSDDLVTIMLYYTKR 240

QY 181 ELXPRIGKSDIVFTNCRGMMKSAVLAITYCIKOYEINGKYSDDLVTIMLYYTKR 240
 DB 181 ELXPRIGKSDIVFTNCRGMMKSAVLAITYCIKOYEINGKYSDDLVTIMLYYTKR 240

QY 241 FPMWEGVYNTMDIAHDSGEFYICMGCLVWVPSVYSPGYLVNHNVEIGTOLATYTLVA 300
 DB 241 FPMWEGVYNTMDIAHDSGEFYICMGCLVWVPSVYSPGYLVNHNVEIGTOLATYTLVA 300

QY 241 FPMWEGVYNTMDIAHDSGEFYICMGCLVWVPSVYSPGYLVNHNVEIGTOLATYTLVA 300
 DB 241 FPMWEGVYNTMDIAHDSGEFYICMGCLVWVPSVYSPGYLVNHNVEIGTOLATYTLVA 300

QY 301 GILCIYINDCDQROREFFRTNGKCLVWGRAPSKIIVASTYTTSGETKTSLLTSGWMWGLA 360
 DB 301 GILCIYINDCDQROREFFRTNGKCLVWGRAPSKIIVASTYTTSGETKTSLLTSGWMWGLA 360

QY 301 GILCIYINDCDQROREFFRTNGKCLVWGRAPSKIIVASTYTTSGETKTSLLTSGWMWGLA 360
 DB 301 GILCIYINDCDQROREFFRTNGKCLVWGRAPSKIIVASTYTTSGETKTSLLTSGWMWGLA 360

QY 361 RHFHYVPEIISAFFWVPALENFPAIFVYFTLLLPDRAKDDDRCSKSGKTKLYC 420
 DB 361 RHFHYVPEIISAFFWVPALENFPAIFVYFTLLLPDRAKDDDRCSKSGKTKLYC 420

QY 361 RHFHYVPEIISAFFWVPALENFPAIFVYFTLLLPDRAKDDDRCSKSGKTKLYC 420
 DB 361 RHFHYVPEIISAFFWVPALENFPAIFVYFTLLLPDRAKDDDRCSKSGKTKLYC 420

QY 421 EK 422
 DB 421 EK 422

RESULT 2
 DHC7_MOUSE
 ID DHC7_MOUSE STANDARD; PRT; 471 AA.
 AC 088455;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 7-dehydrocholesterol reductase (EC 1.3.1.21) (7-DHC reductase) (Sterol
 DE delta-7-reductase).
 GN DHC7.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J;
 RX MEDLINE=96318632; Pubmed=9653161;
 RA Fitzky B.U., Witsch-Baumgartner M., Erdel M., Lee J.N., Paik Y.K.,
 RA Glossmann H., Utermann G., Moebius F.F.;
 RA "Mutations in the delta7-sterol reductase gene in patients with the
 RA Smith-Lemli-Opitz syndrome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8181-8186(1998).
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Production of cholesterol by reduction of C7-C8 double
 RL bond of 7-dehydrocholesterol (7-DHC).
 CC -1- CATALYTIC ACTIVITY: Cholesterol + NADP(+) = cholesta-5,7-dien-3-
 CC beta-ol + NADPH.
 CC -1- PATHWAY: Sterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum.
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
 CC -----
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 CC -----
 DR EMBL: AF057368; AAC40164.1; -;
 DR EMBL: BC006854; AAH06854.1; -;
 DR MGD: MGI:1298378; Dhc7.
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24; 1.
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 KW Sterol biosynthesis; Cholesterol biosynthesis; Oxidoreductase; NADP;
 KM Transmembrane; Endoplasmic reticulum.
 FT TRANSMEM 33 55 POTENTIAL.
 FT TRANSMEM 147 169 POTENTIAL.
 FT TRANSMEM 174 196 POTENTIAL.
 FT TRANSMEM 298 320 POTENTIAL.
 FT TRANSMEM 325 347 POTENTIAL.
 FT TRANSMEM 410 432 POTENTIAL.
 SQ SEQUENCE 471 AA; 53918 MW; 6B1BC356CC39290 CRC64;

Query Match 27.4%; Score 710.5; DB 1; Length 471;
 Best Local Similarity 36.6%; Pred. No. 3.4e-45;
 Matches 157; Conservative 85; Mismatches 158; Indels 29; Gaps 9;

QY 13 ASMSLAFCEPPIVLLMYWHDGCVTQTFGFWEVNGVGLINIMP 60
 DB 13 ASMSLAFCEPPIVLLMYWHDGCVTQTFGFWEVNGVGLINIMP 60

Db 37 ASIFLLPAP--FIVYFIMACDQYSCSLAPALDIATGASHLADIWAKTPPTATANAQ 94
 QY IIFCYGAEATLQLLP-----GKREGEPISPAGNRPYKANGLAAYVT---- 113
 Db 95 LYALMVSFOVLLYSWLPFCRFLPLPGYGVQGEATIPAGVNNKYNGLAMLITHLW 154
 QY 114 -LATYGLGMPFGIENPAIVYDH-IGEIFSALIFSSIFCVLLYTKGHVAPSS--DSSGSC 170
 Db 155 FVNATLLSM---FSPFIIFDNMIPILMVCANILG-YAVSTFAMIKGYLFTPSADCKFTG 209
 QY 171 NLIIDEFWGMELXPRIGSEDIKVFNTNRFMSMAVLAIVYTCIKOIEINKVSDSMLN 230
 Db 210 NEFYVMGIEFNPRIQWPFKEFNCRPPIVAMTILNLSFAKQOELGHVNSMLV 269
 QY 231 TILMLVYTKFEEWAGYVMTMDIAHDRGFIYICMGCLVWPVSYYTSPGMVHPVLG 290
 Db 270 NVLQAIYVLDFFWNTWYLLKIDICHDFGYLNGDCVWLPYITLOGLIVYHPVQLS 329
 QY 291 TQLAIIYVAGILCIYINYDCDROQERRTNGKCLVWGRAPSKIVASYTTSGERTSL 350
 Db 330 TPNALGILLGLVGYIIFRMTNHQKDFRRTDGRCLIMGKPKATECSYTSADGLKHK 389
 QY 351 ILTSGMGLARHVFHVPBILSAFWYVPALENDNLAFYVYVLLFLDRAKDDDCRS 410
 Db 390 LLVSGFWGVARHFNVTGDLMSLAVCIACGGGHLPPFYIITMTLLTHRLRDEHRCAN 449
 QY 411 KYGKWKLY 419
 Db 450 KYGRMERY 458
 RESULT 3
 DHCT_HUMAN STANDARD: PRT; 475 AA.
 ID Q9UBW7: O60492: O60717:
 AC 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE 7-dehydrocholesterol reductase (EC 1.3.1.21) (7-DHC reductase) (Sterol
 delta-7-reductase) (Putative sterol reductase SR-2).
 GN DHCR7 OR D7SR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND VARIANTS SLOS LEU-119; ARG-244 AND CYS-248.
 RX PubMed=9683613;
 RA Waterham H.R., Wijnburg F.A., Hennekam R.C.M., Vreken P.,
 RA Poll-The B.T., Doriand L., Duran M., Jila P.E., Smeitink J.A.M.,
 RA Wevers R.A., Wanders R.J.A.;
 RT "Smith-Lemli-Opitz syndrome is caused by mutations in the
 RT 7-dehydrocholesterol reductase gene.";
 RL Am. J. Hum. Genet. 63:329-338(1998).
 RN [2]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC TISSUE=Liver;
 RX MEDLINE=98132689; PubMed=9465114;
 RA Moebius F.F., Fitzky B.U., Lee J.N., Paik Y.K., Glossmann H.,
 RT "Molecular cloning and expression of the human delta7-sterol
 RT reductase.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:1899-1902(1998).
 RN [3]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=99097347; PubMed=9878250;
 RA Holmer L., Pezhaman A., Norman H.J.;
 RT "The human lamin B receptor/sterol reductase multigene family.";
 RL Genomics 54:469-476(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.

RN [5]
 RP SEQUENCE OF 14-475 FROM N.A.
 RC TISSUE=Liver;
 RX PubMed=9634533;
 RA Wassif C.A., Maslen C., Kachilele-Linjeweile S., Lin D., Linck L.M.,
 RA Conner M.E., Steiner R.D., Porter F.D.;
 RT "Mutations in the human sterol delta 7-reductase gene at 11q12-13
 RT cause Smith-Lemli-Opitz syndrome.";
 RL Am. J. Hum. Genet. 63:55-62(1998).
 RN [6]
 RP VARIANTS SLOS S-51; M-93; P-99; P-157; V-247; I-326; W-352; S-380;
 RP C-404 AND S-410.
 RX MEDLINE=98318632; PubMed=9653161;
 RA Fitzky B.U., Witsch-Baungartner M., Erdel M., Lee J.N., Paik Y.-K.,
 RA Glossmann H., Utermann G., Moebius F.F.;
 RT "Mutations in the delta7-sterol reductase gene in patients with the
 RT Smith-Lemli-Opitz syndrome.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:8181-8186(1998).
 RN [7]
 RP VARIANT SLOS ILE-289.
 RX PubMed=10995508;
 RA Krakowiak P.A., Nwokoro N.A., Wassif C.A., Battaille K.P.,
 RA Nowaczyk M.J.M., Connor W.E., Maslen C., Steiner R.D., Porter F.D.;
 RT "Mutation analysis and description of sixteen RSH/Smith-Lemli-Opitz
 RT syndrome patients: polymerase chain reaction-based assays to simplify
 RT genotyping.";
 RL Am. J. Med. Genet. 94:214-227(2000).
 RN [8]
 RP VARIANTS SLOS MET-93; LEU-326; TRP-352 AND CYS-404.
 RX PubMed=11175299;
 RA Witsch-Baungartner M., Ciara E., Löffler J., Menzel H.J., Seedorf U.,
 RA Burn J., Gilleßen-Kaesbach G., Hoffmann G.F., Fitzky B.U., Mundy H.,
 RA Clayton P., Kelley R.I., Krajewska-Watasek M., Utermann G.,
 RT "Frequency gradients of DHCR7 mutations in patients with Smith-Lemli-
 RT Opitz syndrome in Europe: evidence for different origins of common
 RT mutations.";
 RL Eur. J. Hum. Genet. 9:45-50(2001).
 CC -1- FUNCTION: Production of cholesterol by reduction of C7-C8 double
 CC bond of 7-dehydrocholesterol (7-DHC).
 CC -1- CATALYTIC ACTIVITY: Cholesterol + NADPH(+) = cholesta-5,7-dien-3-
 CC beta-ol + NADPH.
 CC -1- PATHWAY: Cholesterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum.
 CC -1- TISSUE SPECIFICITY: Most abundant in adrenal gland, liver, testis,
 CC and brain.
 CC -1- DISEASE: Defects in DHCR7 are the cause of Smith-Lemli-Opitz
 CC syndrome (SLOS or SLO). SLOS is a frequent inborn disorder of
 CC sterol metabolism with characteristic congenital malformations and
 CC dysmorphias. All patients suffer from mental retardation. Children
 CC with SLOS have elevated serum 7-dehydrocholesterol (7-DHC) levels
 CC and low serum cholesterol levels. SLOS occurs in relatively high
 CC frequency: approximately 1 in 20,000 to 30,000 births in
 CC populations of northern and central European background.
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
 CC
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 CC
 CC EMBL: AF096305; AAD09766.1; -
 CC EMBL: AF034544; AAC05086.1; -
 CC EMBL: AF110060; AAD24762.1; -
 CC EMBL: AF067127; AAD02816.1; -
 CC EMBL: BC000054; AAH00054.1; -
 CC EMBL: AF062481; AAC18345.1; -
 CC Genew: HGNC:2860; DHCR7.
 CC MIM: 602858; -
 CC MIM: 270400; -

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DR MIM: 268670;
DR InterPro: IPR001171; ERG4_ERG24.
DR Pfam: PF01222; ERG4_ERG24; 1.
DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
DR Sterol biosynthesis; Cholesterol biosynthesis; Oxidoreductase; NADP;
KW Transmembrane; Endoplasmic reticulum; Disease mutation.
FT TRANSMEM 37 59
FT TRANSMEM 151 173
FT TRANSMEM 178 200
FT TRANSMEM 264 286
FT TRANSMEM 332 354
FT TRANSMEM 414 436
FT TRANSMEM 51 51
FT VARIANT 93 93
FT VARIANT 99 99
FT VARIANT 119 119
FT VARIANT 157 157
FT VARIANT 244 244
FT VARIANT 247 247
FT VARIANT 248 248
FT VARIANT 289 289
FT VARIANT 326 326
FT VARIANT 352 352
FT VARIANT 380 380
FT VARIANT 404 404
FT VARIANT 410 410
FT CONFLICT 5 5
FT CONFLICT 14 14
SQ SEQUENCE 475 AA; 54489 MW; 7D726443834C4EEB CRC64;

Query Match 26.9%; Score 698.5; DB 1; Length 475;
Best Local Similarity 35.3%; Pred. No. 2.6e-44;
Matches 154; Conservative 87; Mismatches 152; Indels 43; Gaps 10;

13 ASMLSLAFCPPVILMYMHQD-----GSVTQTEGFEWENGVOGLINIW--PPR 62
14 ASVIFLLLPF---FIYYITMACDDQYSCALIGPVVDI---TGHARLSDIMAKTPPI 92
63 TLIAKTIIFCYGAEALLOLLP-----GKRVGSPISPAENRPPYKANGLAAYF 111
93 TRRAAQLYTLWTFGVLYLSLDPFCHKLPYGVGSIQEAAPVPAQVYKNGYQINGQAWL 152
112 VTLATYLGWLF-----GIENPAIYVDH-IGEIFSALIFGSPITFCVLLYINGHVASPS 164
153 LT-----HLMEFANAILLSFSPITIFDWTPLKCANILG-YAVSTFPAWKGFFPTTA 206
165 -DSGSGCNLLIIEYWNELPRIGKSFDIKFTNCRGMSMAVAIAVYCIKOYEINGKV 223
207 RCKKFGNFYNYMGMIEFNPRIKGMDFELFNGRGPVIAWTLINLSFAAQRELHSHV 266
224 SDSMLVNTIIMLYVTKFWEWEGYNTMDIADRGCFITCMGCLVWVSVTSPMTLY 283
267 TNAVAVNVNLAIVYIDFEWNEFWYLTIDICDHFGVWGCWMLPYLYTLQGLYLV 326
284 NHVEVLTQAIYIIVAGILCIYINDCQROREPRRTNGKCLYMGARASKIVASTTTS 343
327 YHPOVSTPRAVGVLLGLVGYIIFRYVANHQKDLFRRTDGRCLIMGKRKPRVLECYTSAD 386

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QY 344 GETKSLTSLTSGMWGLARHHEHYVPEILSAFEWYPAIDFNELVYFYIFLLTFDAKR 403
DB 387 GORHRSKLVSGFVGVARHRYVVDIMGSLAYCAGGGHLLPRFYIYMAILLTLCUR 446
QY 404 DDDRCKSYGKYWKLY 419
DB 447 DEHRCASKYGRDWERY 462

RESULT 4
LBR_CHICK STANDARD; PRT; 637 AA.
AC P23913;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lamin B receptor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91009487; PubMed=2170422;
RX "Worman H.J., Evans C.D., Blobel G.;
RT "The lamin B receptor of the nuclear envelope inner membrane: a
RL J. Cell Biol. 111:1535-1542(1990).
CC -1 FUNCTION: ANCHORS THE LAMINA AND THE HETEROCHROMATIN TO THE INNER
CC NUCLEAR MEMBRANE. CAN INTERACT WITH CHROMODOMAIN PROTEINS.
CC -1 SUBCELLULAR LOCATION: NUCLEAR ENVELOPE INNER MEMBRANE.
CC -1 PM: UNDERGOES PHOSPHORYLATION BY CDC2 PROTEIN KINASE IN MITOSIS
CC WHEN THE INNER NUCLEAR MEMBRANE BREAKS DOWN INTO VESICLES THAT
CC DISSOCIATE FROM THE LAMINA AND THE CHROMATIN. IT IS PHOSPHORYLATED
CC BY DIFFERENT PROTEIN KINASES IN INTERPHASE WHEN THE MEMBRANE IS
CC ASSOCIATED WITH THESE STRUCTURES. PHOSPHORYLATION OF LBR AND HPL
CC PROTEINS MAY BE RESPONSIBLE FOR SOME OF THE ALTERATIONS IN
CC CHROMATIN ORGANIZATION AND NUCLEAR STRUCTURE WHICH OCCUR AT
CC VARIOUS TIMES DURING THE CELL CYCLE.
CC -1 SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
CC -----
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CC -----
DR EMBL: Y00822; CA668758.1; -.
DR PIR: A36427; A36427.
DR InterPro: IPR001171; ERG4_ERG24.
DR InterPro: IPR002999; Tudor.
DR Pfam: PF01222; ERG4_ERG24; 1.
DR SMART: SM00333; TUDOR; 1.
DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
KW Receptor; Transmembrane; Phosphorylation; Nuclear protein;
KW DNA-binding.
FT DOMAIN 1 205
FT TRANSMEM 206 226
FT TRANSMEM 250 270
FT TRANSMEM 288 309
FT TRANSMEM 317 338
FT TRANSMEM 378 399
FT TRANSMEM 403 425
FT TRANSMEM 466 486
FT TRANSMEM 554 574
FT MOD_RES 95 95
FT MOD_RES 96 96
SQ SEQUENCE 637 AA; 73497 MW; 69D299002DB8EC0 CRC64;

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Db 424 NS-FOLLVVDALMNEALLTMDIHDGFMALGDLVWPFIYSFOAFYLVSHNVEY 482
 QY 290 GFOALAIYIIVAGILCIYIN-DCDROROEFRRTNGKCLVGRAPSKIVASYTTGETKT 348
 Db 483 SPMASALITVLK-LCGVIFRGANSOKNAFRK-----PSPKLAHLKTHITSTG 531
 QY 349 SLLTSGMGLARHFFHYVPELLSAFFWYPALFDNFLAYFYVIFLTLFDRARDDDC 408
 Db 532 KNLVSGMGVGFHNPVLDGLMALMSLPCGFNHLPEFYIIFMLVHREARDEYHC 591
 QY 409 RSKYGYWKIYCKE 422
 Db 592 KKKYGVAMEKYYCOR 605

RESULT 6

ER24_ASCIM STANDARD: PRT: 430 AA.
 ID ER24_ASCIM
 AC P78575;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
 GN ERG3.
 OS Ascombolus immerus.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Pezizomycetes;
 OC Pezizales; Ascombolaceae; Ascombolus.
 OX NCBI_TaxID=5191;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=RM42;
 RA Kasbekar D.P.;
 RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REDUCES THE C14-C15 DOUBLE BOND OF 4,4-DIMETHYL-
 CC CHOLESTA-8,14,24-TRIENOL TO PRODUCE 4,4-DIMETHYL-CHOLESTA-8,24-
 CC DIENOL. (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,24-dien-3-
 CC beta-ol + NADP(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-
 CC beta-ol + NADPH.
 CC -1- PATHWAY: Ergosterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
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 CC
 CC EMBL: Y10624; CAA71650.1;
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24; 1.
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 KW Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane.
 FT TRANSMEM 12
 FT TRANSMEM 32
 FT TRANSMEM 67
 FT TRANSMEM 87
 FT TRANSMEM 109
 FT TRANSMEM 129
 FT TRANSMEM 230
 FT TRANSMEM 250
 FT TRANSMEM 267
 FT TRANSMEM 287
 FT TRANSMEM 290
 FT TRANSMEM 310
 FT TRANSMEM 349
 FT TRANSMEM 369
 FT TRANSMEM 376
 FT TRANSMEM POTENTIAL.
 SQ SEQUENCE 430 AA; 49126 MW; 7A61F01A4701B59D CRC64;

Query Match 19.4%; Score 503.5; DB 1; Length 430;

Best Local Similarity 31.7%; Pred. No. 5e-30; Mismatches 140; Conservative 67; Mismatches 175; Indels 59; Gaps 15;

QY 8 PIVTASMLSLAFPCPFVILLWYTWVHODGSGVTFGFFWENGVLINIMPR-----PT 63

Db 11 PIGTGLMLIL-----PPISHYLFHLTPRGAPPE-----FWSADLETLKSVTPFSSLS 62
 QY 64 LIAMKIIFCYGAFAEIIIDLLPGKRVESPISPAGNRPYKANGIAAFVYLATYLG----- 119
 Db 63 LHATLAVAAYVLLVVALMYLPALAEAGVVLKDSRLKRCRANFTT-FLVEFFVLGMV 121
 QY 120 ----LMMGIFNPFAIVYHLEIFESALIFGIFCVLLYIGH-VAPSS-----SDSGSC 169
 Db 122 LEGPTWFMFMSY-----LIDNFAQLOSASIVFYSAMSLWYIRISYPMKRGVILSPGFK 177
 QY 170 GNLLIDFYGMELYPRIKSFIDIVFTNCRFGMSMAVLAATYCIKOYEINGKYSMDLV 229
 Db 178 GNHIDFWMGRELNPRIGEIMLDIKOLHELRLGLMGILFNLAMTVKQYNTHGFEVSDSIVL 237
 QY 230 NTIIMLVYVTFEWFWEAGYNTMDIAHGRGFYICMGCLVWVPSVYSPGKYLVNHYEL 289
 Db 238 VNLFEPTWYVVDALMNEKSVLTFTMDITDGLVMLFLGNAVWPPVYCLQARYLASFPVHL 297
 QY 290 GFOALAIYIIVAGILCI-YIN-----DCDROROEFRRTNGKCLVGRAPSKIVASY-----T 340
 Db 298 G-----LGIAGVLAVOPTGTAIRGANNOXNAF-RTN-----PADRAVSHLFTMT 342
 QY 341 TTSGEFTKSTLLTSGMGLARHFFHYVPELLSAFFWYPALFDNFLAYFYVIFLTLFDR 400
 Db 343 TKSG-----SKLLISGMGVARHNVVFGDWMVMSYCLTGTGNTPLTFYVYIFGILLHR 398
 QY 401 AKRDDDRCKRYGKYWKIYCE 421
 Db 399 DRRDEAKCRKRYGKDWDRYCK 419

RESULT 7

ER24_SCHPO STANDARD: PRT: 424 AA.
 ID ER24_SCHPO
 AC Q09195;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
 GN ERG24 OR SPBC1655.18.
 GN Schizosaccharomyces pombe (Fission yeast).
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 OX NCBI_TaxID=4896;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=SP66;
 RA MEDLINE=95212923; Pubmed=7698661;
 RA Smith S.;
 RT "Cloning and sequence analysis of an ERG24 homolog from
 RT Schizosaccharomyces pombe.";
 RL Gene 155:139-140(1995).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; Pubmed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltrielli T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds N.G., Squares R., Stevens S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Voiclaert G., Aert R., Roben J., Gymnopoulos B.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lebrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Jelaire V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Galliard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombe W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*.";
 RL Mature 415:871-880(2002).
 CC -1- FUNCTION: REDUCES THE C14=C15 DOUBLE BOND OF 4,4-DIMETHYL-
 CC CHOLESTA-8,14,24-TRIENOL TO PRODUCE 4,4-DIMETHYL-CHOLESTA-8,24-
 CC DIENOL (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,24-dien-3-
 CC beta-ol + NADPH(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-
 CC beta-ol + NADPH.
 CC -1- PATHWAY: Ergosterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
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 CC -----
 DR EMBL; L36039; AAA1421.1; -;
 DR EMBL; AL023554; CA119037.1; -;
 DR InterPro: IPR001171; ERG4-ERG24.
 DR Pfam: PF01222; ERG4-ERG24; 1
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 DR Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane.
 FT TRANSMEM 19 39 POTENTIAL.
 FT TRANSMEM 112 132 POTENTIAL.
 FT TRANSMEM 370 390 POTENTIAL.
 SO SEQUENCE 424 AA; 48560 MW; 1D3CE704F1B5E5B CRC64;
 Query Match 19.3%; Score 500.5; DB 1; Length 424;
 Best Local Similarity 32.5%; Pred. No. 8,1e-30;
 Matches 128; Conservative 67; Mismatches 172; Indels 27; Gaps 11;
 43 TFGFENGNGVGG-----LIMMPRTLLAMKIIICFYGAFAILLQLL---LGGKRYEG- 91
 32 SFGSEFYICNEGGCPAKFSKISHIKPTPLDOKSLILYLLMFSTLLMLMCKTGKNAKGT 91
 92 PISPAGNRPPYKANGL-AAFVTLATYGLMFGIFNPDAIVDH-LGEISALIFGSEIF 149
 92 PIDDKGRLLKYKINGFSACLLIGVCTSYLLGASCMETINDFQLQMAAIVF-SVVL 150
 150 CVLLIKYGHVAPSS-SDSGSCGNIIDFYGMELYPRIKSPDIFKVTNCRGMSMAVL 208
 151 CTFCYVOSFEGKQDLAKGTSGNILFDMFGRSLNPRIG-NPDIKFCFCELRPLILMAYVE 209
 209 AVMYCIKQY-EINGKYSDSLVTMTLLMYYVTFEWMGAGYNTMTDIAHGRGFYICWG 267
 210 DIFACQIYLVGRITDSWVLIIFHTFWVDSLINESAVLTMTITDGGFYMSFGD 269
 268 LVWVPYVTVSPGMYLVNHPPELTQALYILVAGIICITVINYDCROROFRRITNGKCIY 327
 270 LVWVPFLYSQARLAFHPVDLGLVKTALICLOPLGIYIFFRANOKNFRBNPD--- 326
 328 WGRAPSVIVASTYTTSETTSLLLSGWMGLARHHPYELLISAFETWVPALEDFNLAY 387
 327 ----PKLKHUKFTQTKRGTR---LLTSGWGMARHINVEGDMIMAWMCLPAGFGSIPY 379
 388 FYVYFLTLFLFDRAKRDDDCRSKYGYKWLCE 421
 380 FYVAYEGVLLVHRNARDHRCRKYKVEDMEKYCK 413

RESULT 8
 ID ER24_HUMAN STANDARD; PRT; 418 AA.
 AC 076062; 095982; 096621; 09664;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
 DE (Sterol C14-reductase) (Delta14-SR) (Transmembrane 7 superfamily
 DE member 2) (Another new gene 1) (Putative sterol reductase SR-1).
 GN TW7SF2 OR ANGI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=98277456; PubMed=9615229;
 RA Lemmens I.H., Kas K., Merregaert J., Van De Ven W.J.M.;
 RT Identification and molecular characterization of TW7SF2 in the FAUNA
 RL gene cluster on human chromosome 11q13.";
 RN Genomics 49:437-442(1998).
 RN [2]
 RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
 RX MEDLINE=9907347; PubMed=9878250;
 RA Holmer L., Pezhman A., Worman H.J.;
 RT "The human lamin B receptor/sterol reductase multigene family.";
 RL Genomics 54:469-476(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain, and Eye;
 RA Strausberg R.;
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP FUNCTION.
 RX PubMed=11784322;
 RA Roberti R., Bannati A.M., Galli G., Caruso D., Maras B., Aisa C.,
 RA Beccari T., Della Faglia M.A., Servillo G.;
 RT "Cloning and expression of sterol Delta14-reductase from bovine
 RT liver.";
 RL Eur. J. Biochem. 269:283-290(2002).
 CC -1- FUNCTION: Involved in the conversion of lanosterol to cholesterol.
 CC -1- CATALYTIC ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,24-dien-3-
 CC beta-ol + NADPH(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-
 CC beta-ol + NADPH.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic
 CC reticulum.
 CC -1- TISSUE SPECIFICITY: Expressed in adult heart, brain, pancreas,
 CC lung, liver, skeletal muscle, kidney, ovary, prostate, and testis,
 CC but not detected in placenta, spleen, thymus, small intestine,
 CC colon (mucosal lining), or peripheral blood leukocytes.
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
 CC -1- CAUTION: Ref.1 sequence differs from that shown due to a number of
 CC sequencing problems as reported in Ref.2.
 CC -----
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 CC -----
 DR EMBL; AF048704; AAC21457.1; ALT_FRAME.
 DR EMBL; AF023676; AAC21450.1; ALT_FRAME.
 DR EMBL; AF096303; AAD09769.1; -;
 DR EMBL; AF096304; AAD09765.1; -;
 DR EMBL; BC009052; AAD09052.1; -;
 DR EMBL; BC012857; AAH12857.1; -;
 DR EMBL; BC012857; AAH12857.1; -;
 DR Genew; HGNC:11863; TW7SF2.
 DR MIM: 603414; -;

DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24; 1.
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 DR Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane;
 KW Endoplasmic reticulum; Polymorphism.
 FT TRANSMEM 13 35 POTENTIAL.
 FT TRANSMEM 62 81 POTENTIAL.
 FT TRANSMEM 102 124 POTENTIAL.
 FT TRANSMEM 129 148 POTENTIAL.
 FT TRANSMEM 255 277 POTENTIAL.
 FT TRANSMEM 287 304 POTENTIAL.
 FT TRANSMEM 355 377 POTENTIAL.
 FT VARIANT 299 299 I->T.
 FT /FTID=VAR.012716.
 FT CONFLICT 179 179 L->V (IN REF. 3: AAH12857).
 SO SEQUENCE 418 AA; 46417 MW; 357C8ABE2BED918 CRC64;
 Query Match 19.3%; Score 499.5; DB 1; Length 418;
 Best Local Similarity 32.8%; Pred. No. 9.5e-30;
 Matches 123; Conservative 60; Mismatches 167; Indels 25; Gaps 8;
 QY 54 GLINTPPTLLAMKLIIFCYGAFAEALQLLLPGKRVGSPISAGKRPVYKANGLAAYFT 113
 DB 53 GLEVLMSPRALLIW--LAMLGLQALYLLLPARKVAEGGELKDKSRRLRPINGQALVLT 109
 QY 114 LNTYGLMWFGLFNPAYVDHGEIPEALIF---GSFICVLLYIKGVAPSS--SDSG 167
 DB 110 -ALLVGLG---MSAGLPGLALPEMLPLAFATLTAFTFSFLYMKQAVAYSLAERG 164
 QY 168 SCGNLIIDFYWGMELYPRIGKSPDIKVTNCRFGMMAMAVLYVCIKOYEINGKVSQM 227
 DB 165 NSGNPIYDFELGRELNPRI-CEPDFKFCFELRGLIGVLLINLALMKRAELRGSPSLAM 223
 QY 228 LVNTIIMLYVYKFFWMEGQYNTMDIAHNRGFTYICAGCLVAVSVYISPMYLVNHPV 287
 DB 224 WLVNGFOLLVYGDALMHEBAVLITMDITHDGCFMLAFGDMAWVPTYSLOAQFLIHQO 283
 QY 288 ELGTOLATYIVAGILCIYINDDOROEPRFTNGKCLVWGRAPSKIVASYTTTSGETK 347
 DB 284 PLGLPRAVSYICLINAIGYITFGANSOKMTFRKNPSDPVAG-----LETSTATGR- 336
 QY 348 TSLILTSQWGLARHFRHYVPEILSAFFWTVPALFDNFLAYFYVIELLLFRKRDDDR 407
 DB 337 ---LTVSGWGMVRRHNPVIGDILMALWSLPCGVSHLLPYFYLVTALLVREARDEQ 393
 QY 408 CRKSYGKRYKLYCEK 422
 DB 394 CLOKYGILAOEYCR 408
 RESULT 9
 ER24_NEUCR STANDARD: PRT: 490 AA.
 AC P38670;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
 DE (Sterol C14-reductase).
 GN ERG-3 OR ERG3.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=74-OR23-1A;
 RA Papavinasandaram K.G., Kasbekar D.P.;
 RT "The Neurospora crassa erg3 gene encodes a protein with sequence
 RT homology to both yeast sterol C-14 reductase and chicken lamin B
 RT receptor.";
 RL J. Genet. 73:33-41(1994).

CC -1- FUNCTION: REDUCES THE C14=C15 DOUBLE BOND OF 4,4-DIMETHYL-
 CC CHOLESTA-8,14,24-TRIENOL TO PRODUCE 4,4-DIMETHYL-CHOLESTA-8,24-
 CC DIENOL.
 CC -1- CATALYTIC ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,24-dien-3-
 CC beta-ol + NADPH(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-
 CC beta-ol + NADP.
 CC -1- PATHWAY: Ergosterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
 CC -----
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 CC -----
 DR EMBL: X7795; CA54919.1; -.
 DR PIR: S44170; S44170.
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24; 1.
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 KW Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane.
 FT TRANSMEM 23 43 POTENTIAL.
 FT TRANSMEM 80 100 POTENTIAL.
 FT TRANSMEM 136 156 POTENTIAL.
 FT TRANSMEM 160 180 POTENTIAL.
 FT TRANSMEM 230 250 POTENTIAL.
 FT TRANSMEM 255 275 POTENTIAL.
 FT TRANSMEM 324 344 POTENTIAL.
 FT TRANSMEM 436 456 POTENTIAL.
 SO SEQUENCE 490 AA; 54722 MW; 9CF3104EF3014085 CRC64;
 Query Match 18.3%; Score 473.5; DB 1; Length 490;
 Best Local Similarity 30.9%; Pred. No. 9e-28;
 Matches 133; Conservative 61; Mismatches 151; Indels 85; Gaps 18;
 QY 48 W-ENGVOGLINMPRLTAMKLIIFCYGAFAEALQLLLPGKRVGSPISAGNRPVYKANG 106
 DB 75 WPDNGVGLNS-W--SATLWTL--GYALSIVYRRLPGHHVGTSLSGGRKLYKLA 128
 QY 107 LAAYVTLATYLG-----LMWGFNPAYVDHGEIPEALIFGFIICVLLYIK 156
 DB 129 FNSACLTALIAAGTIAOGAEFPVWF-----ISDNFAQIISANILFAFALAIFYVR 181
 QY 157 G-HVAPSSD-----SGSGCNLIIDFYWGMELYPRIG---KSPDIKVTNCRFGMSV 205
 DB 182 SFDVKPGKMDKRLAAGGVGSLIYDFYIGRELNPRLITPLIGOVDIKEFMENPGLLGW 241
 QY 206 AVLAVTYCIRQYEINGKVSQSMNVNTIIMLYVYKFFWMEGQYNTMDIAHNRGFTYICW 265
 DB 242 IILNCAPIAKQYRLXGVYTDLSILFTIAQAFYVDGIYMEVAVLITMDITTDGCFMLSF 301
 QY 266 GCLVWVPSVYTPSPMYLVNHEVELGT--QLAI-YLVAGILCIYINDDOROEPRFTN 322
 DB 302 GDVWVWPPMYSTQYRILSVHPQGLGAFGLAVGAVLAAGSIFRLS--NSQKNF--RTN 357
 QY 323 GKCLVWGAAPKIVASYTTTSGETKT-SLLTSGWGLARHFRHYVPEILSAFFWTVP--- 378
 DB 358 PE-----DPSVKHLTYL---QRTKTSRLITSGWGIARHINILGWLDSWPSLPTGI 407
 QY 379 -----ALFDN-----FLAFYVIELLLFRKRDDDR 409
 DB 408 AGYQLLSAGSNAPGALITMLDREVVOGEARGWGIYFYFYLITLIRDLKDDKCS 467
 QY 410 SKYGYKRYLY 419
 DB 468 KKYGDWMEKY 477
 RESULT 10

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CC -----
DR EMBL; AF26535; AAF8282.1; -
DR EMBL; AF26536; AAF8283.1; -
DR EMBL; AF257178; AAF81279.1; ALT_INIT.
DR EMBL; AF263244; AAF82768.1; -
DR EMBL; ALI32969; CAC01296.1; ALT_INIT.
DR InterPro; IPRO01171; ERG4_ERG24.
DR Pfam; PF01222; ERG4_ERG24; 1.
DR PROSITE; PS01017; STEROL_REDUCT_1; 1.
DR PROSITE; PS01018; STEROL_REDUCT_2; 1.
KW Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane.
FT TRANSMEM 15 34 POTENTIAL.
FT TRANSMEM 54 76 POTENTIAL.
FT TRANSMEM 86 105 POTENTIAL.
FT TRANSMEM 146 168 POTENTIAL.
FT TRANSMEM 178 195 POTENTIAL.
FT TRANSMEM 208 230 POTENTIAL.
FT TRANSMEM 240 262 POTENTIAL.
FT TRANSMEM 275 297 POTENTIAL.
FT TRANSMEM 317 336 POTENTIAL.
SQ SEQUENCE 369 AA; 41913 MW; F18674BC27C0502 CRC64;

Query Match 18.1%; Score 470.5; DB 1; Length 369;
Best Local Similarity 32.2%; Pred. No. 1.1e-27;
Matches 120; Conservative 79; Mismatches 131; Indels 43; Gaps 14;

QY 62 PTLAMKIFICYGAPFALQLLLDPGRKEGPIISPAGNRPYKANGLAAYFVLTATYGLW 121
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 12 PLSLSVYVLYVFYFYLVAAGELLPKGIKRGVLLSDGSLRYRCGLLA-LILLVALIGIC 70
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 122 -WGIENFAIYYDHLGEFFSLIFGSIFFCYL---LYIKGHVAPSSSDSGS-----CG 170
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 71 AKGLIVSLVYVADGDELISA-----TFICVLYLTALTYGR---SSNKGSSLIKPHVSG 123
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 NLIIDFVGMELVYPRIGKSFDIKVFYTCRGFGMSMAVLAVTYCIKQYEINGKVSQMLVN 230
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 124 NLVHDWFFGIQIDNQF-MSIDLKFEFF-VRAQMGWLLINISILAKSVQ-DGSLQSMTLY 180
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 231 TILMLVYVTKFEMWAGVWNTMDIAHGRGFGYIOMGCLVWVPSVYTSQWLYVHHPYELG 290
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 181 QIFCALVILDFYVDEEYVTSIWDIIAEELGMLVFQGLMLPTFFSIQGMWLLHNKVE-- 238
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 291 TQALVYLVAIGLICITINY----DCDRQDEFRRTNGKCLVWGRAPSKIVASYTTSGET 346
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 239 --LHVPAIVVNCVLFELIGYVFRGANKOKHFKK-NPKTPIMGRP-----VVGSGK- 287
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 347 KTSILLNSGMGGLARHRYHVPSELLSAFFWYPALEDFNLAIFYIFLTLLFDPAKRDD 406
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 288 ----LLVSGVIGIARHCHVIGDMLALSLFSLPCGISSPVPEFYIYLLIILWRRDEY 343
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 407 RCRSKYGRKMYKLY 419
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ 344 RCAEKYKEIMAEY 356
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
ID ER24_FUSSO STANDARD; PRT; 485 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
OS Fusarium solani (subsp. pisi) (Nectria haematococca);

```


Db 145 VTIFVACAGTIVRGPEQWTF-----INRNYQLTWNIIIAVALIYYLKSEV 197
 Qy 161 PSSSD-----SGSGCNLIIDFEWGMELPRICKSF-----DIKVFNCFGMAAVLA 209
 Db 198 KAGTEORELAAGSHSHLLIYDWGRELNRITPTTIPGEVDIKSFELPFGMIGWLLD 257
 Qy 210 VTTCIKOYEINGKVSMSLVNTIIML-----VYVVKFFWMEAGYWNMT 252
 Db 258 LAFAKAKYKSGYITDSMRKWTPLLLGIVLTHPIVVIISQSYVVDALYMEPAITTM 317
 Qy 253 DIANDRGFEIYCWGLVWDSVYTSPOGMVYVNHVELGTOLAIYILVAGILCIYNYDCD 312
 Db 318 DLITDGGFMISFEDLVWVPEIYSIQAKYLSVHVALGSPYVALITLQATGYI----- 372
 Qy 313 RQREFRRTGKCLVWRARASKIYASTTTSGETKTSLLTSGMWGLARHPHYVPELISA 372
 Db 373 -----FPAIINDKNIFPTNPDPKVAHLKXIETGTGSRLLTGGWGAHINVLGMLMS 427
 Qy 373 FFWTVPA-----LFDNF-----LAFYVYFLLTLLFDRAKRDDR 407
 Db 428 WSYCLPFLAAGYKLTPLTLPENSRLVSTDGMKAGIPITYFYMLYFAILLHRRDEAK 467
 Qy 408 CRKRYGKYMKLYCE 421
 Db 488 CRKRYGAHWEKCYQ 501

RESULT 13

ER24_YEAST STANDARD; PRT; 438 AA.
 ID ER24_YEAST STANDARD; PRT; 438 AA.

AC P32462;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta(14)-sterol reductase (EC 1.3.1.70) (C-14 sterol reductase)
 GN ERG24 OR YNL280C OR NO593.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93039674; PubMed=1418625;
 RA Lorenz R.T., Parks L.W.;
 RT "Cloning, sequencing, and disruption of the gene encoding sterol C-14 reductase in Saccharomyces cerevisiae.";
 RL DNA Cell Biol. 11:685-692(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94171077; PubMed=8125337;
 RA Lai M.H., Bird M., Pierson C.A., Alexander J.F., Goebel M.,
 RT Carter G.T., Kirsch D.R.;
 RT "The identification of a gene family in the Saccharomyces cerevisiae ergosterol biosynthesis pathway.";
 RL Gene 140:41-49(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard A.,
 RL Glandsdorf N.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: REDUCES THE C14-C15 DOUBLE BOND OF 4,4-DIMETHYL-CHOLESTA-8,14,24-TRIENOL TO PRODUCE 4,4-DIMETHYL-CHOLESTA-8,24-DIENOL.
 CC -1- CATALYTIC ACTIVITY: 4,4-dimethyl-5-alpha-cholesta-8,24-dien-3-beta-ol + NADP(+) = 4,4-dimethyl-5-alpha-cholesta-8,14,24-trien-3-beta-ol + NADPH.
 CC -1- ENZYME REGULATION: INHIBITED BY THE MORPHOLINE ANTIFUNGAL DRUG FENPROPIMORPH.
 CC -1- PATHWAY: Ergosterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.

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CC EMBL: M99419; AAA18256.1;
 DR EMBL: S69420; AAB30203.1;
 DR EMBL: 271556; CAA96192.1;
 DR PIR: S30769; S30769.
 DR SGD: S0005224; ERG24.
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24.
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 KW sterol biosynthesis; oxidoreductase; NADP; Transmembrane.
 FT TRANSMEM 14 30
 FT TRANSMEM 72 90 POTENTIAL.
 FT TRANSMEM 110 127 POTENTIAL.
 FT TRANSMEM 148 172 POTENTIAL.
 FT TRANSMEM 243 263 POTENTIAL.
 FT TRANSMEM 309 328 POTENTIAL.
 FT TRANSMEM 369 387 POTENTIAL.
 FT CONFLICT 253 253 L->S (IN REF. 2).
 SQ SEQUENCE 438 AA; 50615 MW; B936B04506C0F3 CRC64;

Query Match 16.4%; Score 424.5; DB 1; Length 438;
 Best Local Similarity 29.7%; Pred. No. 3.2e-24;

Matches 130; Conservative 74; Mismatches 160; Indels 73; Gaps 20;

Qy 23 PPVITLMTWYHODSGYQTFGF-----WENGVO-----GLINIMRPPTLIAMK 68
 Db 28 PVFTIIL-NQMIRPDPYFIK---GFQNPDIVELM-NGIKPLRYLYGNRELW----- 73
 Qy 69 IIFC--YGAFFALIDQLLPGRKVEGPISAGNRPPYKANGLAAYVTLATYIGLMWEGIF 126
 Db 74 TVYCLWYGLI-LAVLDVITLPGRVKMGVQLRDGSKLSYKINGI-AMSTTVLVLAIRMKLTD 131
 Qy 127 N-PAIVY---DHLGEIFSLIFGSEI-----FCVLLYIK---GHVAPSSSDSGSG 170
 Db 132 GOLPELOIYENHVSICILISLFFFLAYCYVASFTPLIFKKNNGKREKILAGMSG 191
 Qy 171 NLIDPEWGMELYPRIKSEFDIKVFTNCRFGMMAVLAIVYCIKOYEINGKVSMSLVN 230
 Db 192 NIITYDFIOTREINPRIG-PLDIKMFSELPKMLMLLNLISLHHYLTGKINDALIV 250
 Qy 231 TILMLVYVTKFFWMEAGYWNMTDIANDRGFEIYCWGLVWDSVYTSPOGMVYVNHVELG 290
 Db 251 NFLQGYIYIDGYLNEBGVLTMDITTDGFGFMALAGDSLVPFTYSLQARVLSVPELG 310
 Qy 291 TOLAIYILVAGILCI-----YNYDCDRQROREFRRTGKCLVWDSVYTSYTTSGE 345
 Db 311 -----WVKVYGLAIIMFELGFHFHSANKOKSEFRG--GKL-----ENKLSIOTKRG- 354
 Qy 346 TYSLLISGMMGLARHPHYVPELISAFETVPALPDNFLAYVITLTLFDRAKRDD 405
 Db 355 TK---LIDGWMWAKSOHINIFGDWILSLSWCATWFOPTLFTYYSLVYATLLHROQDE 411
 Qy 406 DRCRSYKGYMKLYCE 422
 Db 412 HKCRLYGENWEEYERK 428

RESULT 14

ERG4_YEAST STANDARD; PRT; 473 AA.
 ID ERG4_YEAST STANDARD; PRT; 473 AA.

AC P23540;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta(24(24(1)))sterol reductase (EC 1.3.1.71) (Sterol delta(24(28)))

DE reductase) (C-24(28) sterol reductase).
 GN ERG4 OR YGL012W OR YGL022.
 OS Saccharomyces cerevisiae (Baker's Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 RX NCB1_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL125-2B;
 RX MEDLINE=91353085; PubMed=1882555;
 RT Chen W., Caploux E., Balzi E., Goffeau A.;
 RT "The YGL022 gene encodes a putative transport protein.";
 RL Yeast 7:305-308(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL125-2B;
 RX MEDLINE=91353083; PubMed=1882553;
 RA Chen W., Balzi E., Caploux E., Choder M., Goffeau A.;
 RT "The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1
 RT and ATR1 loci on chromosome VII from Saccharomyces cerevisiae reveals
 RT the PDR6 gene, a new member of the genetic network controlling
 RT pleiotropic drug resistance.";
 RL Yeast 7:287-299(1991).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Hebling U., Hofmann B., Delius H.;
 RL Submitted (May-1996) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=94171077; PubMed=8125337;
 RA Lai M.H., Bard M., Pierson C.A., Alexander J.F., Goebel M.,
 RA Carter G.T., Kirsch D.R.;
 RT "The identification of a gene family in the Saccharomyces cerevisiae
 RT ergosterol biosynthesis pathway.";
 RL Gene 140:41-49(1994).
 CC -1- CATALYTIC ACTIVITY: Ergosterol + NADP(+) = ergosta-
 CC 5,7,22,24(24(1))-tetraen-3-beta-ol + NADPH.
 CC -1- PATHWAY: Ergosterol biosynthesis.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE ERG4/ERG24 FAMILY.
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A TRANSPORT PROTEIN.
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 DR EMBL: S58126; AAD13895.1; -
 DR EMBL: S57801; AAI19615.1; -
 DR EMBL: 272534; CAA96712.1; -
 DR PIR: S15042; S15042.
 DR SGD: S0002980; ERG4.
 DR InterPro: IPR001171; ERG4_ERG24.
 DR Pfam: PF01222; ERG4_ERG24.
 DR PROSITE: PS01017; STEROL_REDUCT_1; 1.
 DR PROSITE: PS01018; STEROL_REDUCT_2; 1.
 KW Sterol biosynthesis; Oxidoreductase; NADP; Transmembrane.
 FT TRANSMEM 40 64 POTENTIAL.
 FT TRANSMEM 102 123 POTENTIAL.
 FT TRANSMEM 139 157 POTENTIAL.
 FT TRANSMEM 175 197 POTENTIAL.
 FT TRANSMEM 233 249 POTENTIAL.
 FT TRANSMEM 327 346 POTENTIAL.
 FT TRANSMEM 415 439 POTENTIAL.
 FT TRANSMEM 366 366 G -> V (IN REF. 1 AND 2).
 FT CONFLICT 366 366
 SO SEQUENCE 473 AA; 56039 MW; BABFPI4559272DD6 CRC64;

Query Match 14.3%; Score 371; DB 1; Length 473;
 Best Local Similarity 26.4%; Pred. No. 2.9e-20;
 Matches 115; Conservative 71; Mismatches 202; Indels 48; Gaps 15;

QY 15 MSLALCPPEVILLMTWYMHODGSVT-QTEGFHW-----ENGVOGLINIMPR 61
 Db 46 VIGMLIGPPLMYMMWICAEFYHCKVALPKRGSMMHFIKHVLVLENGI----- 96
 QY 62 PTLIAKKIIFCYGAFAEAILDLPLPKRVEG-PISP-AGNRPVYKANGLAAYVTLATLG 119
 Db 97 PEKYDTWTFLEFWFOILFYFTTLPGIWTGQPLSHLKGKOLPEFCNMMWLYVTTTLVLV 156
 QY 120 LWMGIFPAPVYDHLGEIPLSALLFGSFIICVLLYINGHAPSSDSCGNLIIDPYWG 179
 Db 157 LHFNLFRLLYVYIDFRIRIMCALISGFAPSIILYL-WTLFISHDYHRTGNNHLYDFEMG 215
 QY 180 MEYPRIGKSPDIKFTNCRFGMMAMVAVLYTCIKOYEINGKSDSMLNTIIMLYVT 239
 Db 216 APLNPRMG-IIDDKMFPEVRLPMTLYFTILGACLKOMEYIGYTPDGLVYMLAHMILYAN 274
 QY 240 KFFWMEAGYMTMDIAHDSGGFYICWGLVWPSVYSPGMYLVNH-PVELG----TOLA 294
 Db 275 ACAGGEELIVPTWMAVEKEFGLIFWNINAGVPYTCYCHCTLYLHYHDPSEYHMSLYNVS 334
 QY 295 IYIIVAGLICITYIYVD-CDRQROEFR-----RNGKCLWGRAPSKIVAS--YTTTSGE 345
 Db 335 LYVV---ILCAVYFPDDANAKNAFRKMGSGDKRTFTFP--LPYOLKNPYMTVS-- 387
 QY 346 TKTSLILTSGMWGLARHFFHYPEILISAFMTVPALPFLNFAVFLTLPLDRAKRD 405
 Db 388 -NGSYLLIDGWTYTLARKIHITADWTOSLVNALSGCFNSVFPWFPEVFLVLLHRAFRDQ 446
 QY 406 DRCSKRYGKWKLYCE 421
 Db 447 AKCKRKYGKDWDYCK 462

RESULT 15
 STS1_SCHPO STANDARD; PRT; 453 AA.
 AC P36209; O13891;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Delta(24(24(1)))-sterol reductase (EC 1.3.1.71) (Sterol delta(24(28))-
 DE reductase) (C-24(28) sterol reductase).
 GN STS1 OR SPAC2034.07C.
 OS Schizosaccharomyces pombe (Fission Yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC Schizosaccharomyces.
 RX NCB1_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9232994; PubMed=1320960;
 RA Shimanuki M., Goebel M., Yanagida M., Toda T.;
 RT "Fission yeast sts1+ gene encodes a protein similar to the chicken
 RT lamin B receptor and is implicated in pleiotropic drug-sensitivity,
 RT divalent cation-sensitivity, and osmoregulation.";
 RL Mol. Biol. Cell 3:263-273(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=2184401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayes J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltham T., Fraser A.,
 RA Gentles S., Goebel A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

Db 192 FMGACNPRGLKDLDFKKEFEVR---IPWLFEFISGAVAHQVEYEGVSPQVLFPCLG 248

QY 234 MLVYVYKFFWFMWAGVWNTMDLAHNRGCFYICWGLVWVSUTTSQGMILVNHPEL---G 290

Db 249 HVLVYACSKSGQQLVLPWMDAYEKFGFMLIFWNMAGVPTYSHTCLYLSDSPSVNWS 308

QY 291 TOLAIIVLAGLICLYIYWDQDROREFR---TNGKCLWMBRAPSKVASYT---TTS 343

Db 309 TQYTTIIVYLLLCYIIFDTGNCAGKNFRNQIGTEVHNKTRFQDLWILIKPPTIGCAN 366

QY 344 GETKISLLTSGWMCGLAHNHYVDELLSAEFWTVPALFENFLAYEVYIFLTLIDRAKR 403

Db 369 GGT----LLTSGWYRARKIHYTADFPQSLSMALLTGQSPRYEYGFCEFFVILVHYSR 424

QY 404 DDDRCRSKYGKWKLYC 420

Db 425 DIKCKAKYAGDFDEYC 441

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 14:14:09 ; Search time 22 Seconds
(without alignments)
2079.999 Million cell updates/sec

Title: US-09-817-774-31

Perfect score: 2594

Sequence: 1 MAETVHSPIVTYASMLSLA.....RAKTRMQDAIDILLICML 476

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2312	89.1	432	2 F96540	sterol delta7 redu
2	554	21.4	637	2 A36427	lamin B receptor -
3	553.5	21.3	620	2 JC5567	lamin B receptor -
4	540	20.8	615	2 A53616	lamin B receptor -
5	500.5	19.3	424	2 JC4057	probable C-14 ster
6	473.5	18.3	490	2 S44170	probable C-14 ster
7	424.5	16.4	438	2 S30769	probable C-14 ster
8	418.5	16.1	697	2 T18681	hypothetical prote
9	371.5	14.3	317	2 T47551	nuclear envelope m
10	371	14.3	473	2 S64014	probable transport
11	363.5	14.0	453	2 A43765	stsl+ protein - fi
12	120.5	4.6	524	2 S14138	cytochrome-c oxida
13	118.5	4.6	527	2 S65346	cytochrome-c oxida
14	115.5	4.5	527	2 S14139	cytochrome-c oxida
15	108	4.2	599	2 S67084	probable membrane
16	106	4.1	354	2 C45229	opsin, rod ultravi
17	106	4.1	474	2 S07754	NADH2 dehydrogenas
18	105	4.0	499	2 AH2413	alignate o-acetyl
19	105	4.0	504	2 T04529	probable ammonium
20	104.5	4.0	1418	2 S40764	hypothetical prote
21	104	4.0	444	2 T11474	NADH2 dehydrogenas
22	104	4.0	550	2 H64049	afub protein homol
23	102	3.9	438	1 S24065	preprotein translo
24	101.5	3.9	514	2 T06585	ammonium transport
25	101.5	3.9	522	2 S25956	cytochrome-c oxida
26	101.5	3.9	598	2 S51456	probable membrane
27	101	3.9	494	2 AC0133	probable permease
28	100.5	3.9	485	2 S56559	probable proton/ol
29	100	3.9	438	2 B84919	Not56-like protein

30	100	3.9	485	2 F86108	probable peptide t
31	100	3.9	485	2 H91267	hypothetical prote
32	100	3.9	494	2 F86646	hypothetical prote
33	98.5	3.8	558	2 S08270	cytochrome-c oxida
34	98	3.8	393	2 C95343	hypothetical prote
35	98	3.8	479	2 F86285	F9L1.11 protein -
36	98	3.8	1515	2 T52081	MRP-like ABC trans
37	97.5	3.8	173	2 D58893	NADH2 dehydrogenas
38	97.5	3.8	416	2 G81258	serine transporter
39	97	3.7	443	2 F30010	NADH2 dehydrogenas
40	96.5	3.7	322	2 E84908	hypothetical prote
41	96.5	3.7	333	2 T02690	hypothetical prote
42	96.5	3.7	477	2 D82587	cationic amino aci
43	96.5	3.7	524	1 OD821	cytochrome-c oxida
44	96.5	3.7	528	1 OD821	cytochrome-c oxida
45	96.5	3.7	639	2 T30151	hypothetical prote

ALIGNMENTS

RESULT 1
F96540
sterol delta7 reductase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C:Accession: F96540
R:Rheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chlin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hulzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzla
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: AB6141; MUID:21016719; PMID:11130712
A:Accession: F96540
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-432 <STO>
A:Cross-references: GB:AE005173; NID:g9454565; PID:AF87888.1; GSPDB:GN00141
A:Genetics:
A:Gene: Flr12.21
A:Map position: 1
C:Superfamily: yeast probable C-14 sterol reductase
Query Match 89.1%; Score 2312; DB 2; Length 432;
Best Local Similarity 99.8%; Pred. No. 4.2e-188;
Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MAETVHSPIVTYASMLSLAFCPPVILLIWMVHQDSVTQTFGEFMEVNGVGLINTIP	60
DB	1	MAETVHSPIVTYASMLSLAFCPPVILLIWMVHQDSVTQTFGEFMEVNGVGLINTIP	60
QY	61	RPTLLAMKTIIFCYGAFEAIIQLLPGRKREGISNAGNRPYKAGLAAYVTATATYGL	120
DB	61	RPTLLAMKTIIFCYGAFEAIIQLLPGRKREGISNAGNRPYKAGLAAYVTATATYGL	120
QY	121	WMFGFENPAIVDHLGEISALIFGSFICVLLYTKGVAPSSSDSGSCGNLIIDFYWGM	180
DB	121	WMFGFENPAIVDHLGEISALIFGSFICVLLYTKGVAPSSSDSGSCGNLIIDFYWGM	180
QY	181	EIYPRIGKSFIDIKVFNCRFGMSNAVLAVYTCIKQYEINGKVSQSMLVNTILMIVYTK	240
DB	181	EIYPRIGKSFIDIKVFNCRFGMSNAVLAVYTCIKQYEINGKVSQSMLVNTILMIVYTK	240
QY	241	FWMEGAVNTMDIADHGRGFYICGCLVWVPSYTSQMTLVNHPVDELGQLAITYIYA	300
DB	241	FWMEGAVNTMDIADHGRGFYICGCLVWVPSYTSQMTLVNHPVDELGQLAITYIYA	300
QY	301	GILCIYINDCDROROEFRTNGKCLVWGRAPSKIVASTYTTSGETKTSLLTSGMWGLA	360

```

Db 301 GILCIYINDCORROEFRTNKGKLVWRAPSKIIVASTTTSGEIKTSLILTSQWGLA 360
OY 361 RHFHYPEILSAFTWVPALFDFNFAYFVITLLLPDRAKRDDCRSKYKWKLYC 420
Db 361 RHFHYPEILSAFTWVPALFDFNFAYFVITLLLPDRAKRDDCRSKYKWKLYC 420
OY 421 EK 422
Db 421 EK 422

```

RESULT 2

```

A36427
Lamin B receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 21-Jul-2000
C:Accession: A36427
R:Worman, H.J.; Evans, C.D.; Blobel, G.
J. Cell Biol. 111, 1535-1542, 1990
A:Title: The lamin B receptor of the nuclear envelope inner membrane: a polytopic prote
A:Reference number: A36427; MUID:91009487; PMID:2170422
A:Accession: A36427
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-637 <WOR>
A:Cross-references: GB:Y00822; NID:962933; PIDN:CAA68758.1; PID:962934
C:Keywords: phosphoprotein; transmembrane protein

```

Query Match

```

Best Local Similarity 21.4%; Score 554; DB 2; Length 637;
Matches 138; Conservative 60; Mismatches 179; Indels 40; Gaps 11;

```

```

OY 18 LLAFCPPVILLMTYVHODGSVTQF-----GTFWENGVOGLINIMPRPLIAKTIIF 71
Db 210 MMEFPLPATVLYLMCKODPSIMNFPPLPALESIMETKRVGCVLLM-----FF 259
OY 72 CYGAFEAIIQLLPGRVGE-PISPAQNRPVYKANGLAIFYLATYLGIMWGFNPAT 130
Db 260 ----FQALFTLLPIGKVGESPLSNP-RKIQRINGFYFLTAALIGTLTYFQ-FLHY 313
OY 131 VVDHLGEIFSAIFGSEIFCVLLYIKGHVAPSS--SDSGSCGNLIDFYWGMELYPRIK 188
Db 314 LYDFEVOFAVSAAFSAISLYIRSLKAEEDLAPGNSGLYVDFPTGHELPRIQ- 372
OY 189 SFDIKVFTNCRFGMSMAVLAIVYCIKQYEINGKVSMS---LYNTILMLVYVYKFWME 245
Db 373 SFDIKVFTNCRFGMSMAVLAIVYCIKQYEINGKVSMS---LYNTILMLVYVYKFWME 245
OY 246 AGYWNMTDIAHDROGEFYICWGLVWVPSVYTPGMVYLVNHPVELGTOLAIYILVAGILCI 305
Db 432 EAVLTMTDIIHDGFGFMALFQDLVWVPYYSLOAFYLVGHPRALISMPVAAITILNCIGY 491
OY 306 YINYDCDROGEFRRTNKGKLVWRAPSKIIVASTTTSGEIKTSLILTSQWGLANRHF 365
Db 492 YIFRSANSOKNAPRRN-----PADPKLSYLLKVIPTATGKGLLVGMWGFVHNPY 541
OY 366 YPEILSAFTWVPALFDFNFAYFVITLLLPDRAKRDDCRSKYKWKLYC 422
Db 542 YGDLIMALWSLPCGFNHILPYFYVITFALLIHREARDEHQRKRYGLAMEYCOR 598

```

RESULT 3

```

JCS567
Lamin B receptor - rat
N:Alternate names: nuclear localization signal-binding protein, NBP60
C:Species: Rattus norvegicus (Norway rat)
C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 05-Nov-1999
C:Accession: JCS567; PC4483
R:Kawachi, S.; Takeuchi, M.; Gohshi, T.; Sasagawa, S.; Shimada, M.; Abe,
J. Biochem. 121, 881-889, 1997
A:Title: CDNA cloning of nuclear localization signal binding protein NBP60, a rat homolog
signals and chromatin.

```

```

A:Reference number: JCS567; MUID:97335934; PMID:9192729
A:Accession: JCS567

```

```

A:Molecule type: mRNA
A:Residues: 1-620 <KAW>
A:Cross-references: DDBJ:AB002466; NID:92204061; PIDN:BAA20471.1; PID:d1021305; PID:9
A:Experimental source: Liver
A:Accession: PC4483
A:Molecule type: protein
A:Residues: 2-28;41-50;114-126;153-180;600-619 <KA2>
C:Comment: This protein is the center of perinuclear membrane network on the inner nu
C:Genetics:

```

```

A:Gene: NBP60
C:Keywords: DNA binding; nucleus; phosphoprotein; receptor; transmembrane protein
F:73-99/Region: arginine/serine-rich
F:214-235/Domain: transmembrane #status predicted <TM1>
F:256-283/Domain: transmembrane #status predicted <TM2>
F:301-332/Domain: transmembrane #status predicted <TM3>
F:331-351/Domain: transmembrane #status predicted <TM4>
F:390-411/Domain: transmembrane #status predicted <TM5>
F:415-437/Domain: transmembrane #status predicted <TM6>
F:467-488/Domain: transmembrane #status predicted <TM7>
F:557-587/Domain: transmembrane #status predicted <TM8>

```

```

F:45/Binding site: phosphate (Thr) (covalent) (by calmodulin-dependent kinase II) #st
F:71/Binding site: phosphate (Ser) (covalent) (by cdc2 kinase) #status predicted
F:78/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted
F:123/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status predicted
F:137/Binding site: phosphate (Tyr) (covalent) #status predicted
F:161/Binding site: phosphate (Ser) (covalent) (by calmodulin-dependent kinase II) #s
F:206/Binding site: phosphate (Thr) (covalent) (by cdc2 kinase) #status predicted

```

Query Match

```

Best Local Similarity 21.3%; Score 553.5; DB 2; Length 620;
Matches 138; Conservative 65; Mismatches 176; Indels 39; Gaps 11;

```

```

OY 16 LSLAFCPPVILLMTYVHODGSVTQ-----TFGFWENGVOGLINIMPRPLIAKTI 69
Db 221 LLIMGLPACVFLLLQCAQKDPGLQFPPLPALREIMEARVCGVILLM----- 270
OY 70 IECYGAFAIIQLLPGRVGE-PISPAQNRPVYKANGLAIFYLATYLGIMWGFNPAT 129
Db 271 FF----IQALFSLPLVGVWVGPPLVDGRRLKYLKNGLYAFILISA-VGTAYWMDIELY 325
OY 130 IVDHLEIFSAIFGSEIFCVLLYIKGHVAPSSSDS--GSCGNLIDFYWGMELYPRIK 188
Db 326 YLTHFQLFALAAIVSVLSVLYASRLKVRDELSPASSGNAVDFPTGHELPRIQ- 384
OY 189 SFDIKVFTNCRFGMSMAVLAIVYCIKQYEINGKVSMS---LYNTILMLVYVYKFWME 245
Db 385 AFDKFCELRPGILGVVIVNMLLAEMKVOERSAPSLAATLVNS--FQLLYVVDALMFE 443
OY 246 AGYWNMTDIAHDROGEFYICWGLVWVPSVYTPGMVYLVNHPVELGTOLAIYILVAGILCI 305
Db 444 EAVLTMTDIIHDGFGFMALFQDLVWVPYYSLOAFYLVNHPDLSWPLT-SVITALLCG 502
OY 306 YINYDCDROGEFRRTNKGKLVWRAPSKIIVASTTTSGEIKTSLILTSQWGLANRHF 364
Db 503 YIFRCANSOKNAPRRN-----PTDKLAHLNLTIPSTYKSLVSGMWGFVHNPY 552
OY 365 YPEILSAFTWVPALFDFNFAYFVITLLLPDRAKRDDCRSKYKWKLYC 422
Db 553 YGDLIMALWSLPCGFNHILPYFYVITFALLIHREARDEHQRKRYGLAMEYCOR 610

```

RESULT 4

```

A53616
Lamin B receptor - human
N:Alternate names: LBR
C:Species: Homo sapiens (man)
C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 05-Nov-1999
C:Accession: A53616; A53617
R:Ye, Q.; Worman, H.J.
J. Biol. Chem. 269, 11306-11311, 1994
A:Title: Primary structure analysis and lamin B and DNA binding of human LBR, an inte

```

us-09-817-774-31.rpr

[illegible]

R:Lyne, M.; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Beck, A.; Reinhardt, R.
Submitted to the EMBL data Library, May 1998
A:Reference number: Z21866
A:Accession: T39610
A:Status: preliminary; translated from GB/EMBL/DDJ
A:Molecule type: DNA
A:Residues: 1424 <LNN>
A:Cross-references: EMBL:AL023554; PIDN:CAA19037.1; GSPDB:GN00067; SPDB:SPB016G5.18
A:Experimental source: strain 972h-; cosmid c16G5
C:Genetics:
A:Gene: erg24
A:Map position: 2
C:Superfamily: yeast probable C-14 sterol reductase
C:Keywords: oxidoreductase

Query Match 19.3%; Score 500.5; DB 2; Length 424;
Best Local Similarity 32.5%; Pred. NO. 1.1e-34;
Matches 128; Conservative 67; Mismatches 172; Indels 27; Gaps 11;

```
QY      43 TFGFEWENGVOG-----LINIMPRPTLIAMKIFCYGAFAILOLL--LPGRVEG- 91
```

02 RICHMOND, VA 22101-1000 32 3FG5FYICNEECBPAFRSKISHIFKKTPLPFDKSLIYLLWNESTVLTLMKCTNGKMWAGT 91

Db 92 PIDDGTRLLKINGENSACILIGVCTSYILGASCFEINFLQMLFAAYF-SYVL 150

QY 150 CVLLYTKGVAPSS -SDSGCGLIIDFYWGMELYPRIKSFIDIKVFTNCRFGMSNAVLT 208

D_b 151 CTFCYQSF^{EF}GKQLAKGGSNLPDWF^{IG}SLNPRIG-NEDIKCFCELR^{PG}LIMV^{EF} 209

029 AYTLCIKQY-ELNGKXSDSMVLNTIMLVYYTKFFMWEAGYNNYIMDIAHDRGCFYICWGC 267

268 LWPVPSVYTSQGMYLINHPEVETGTOAIYIIIVAGLICITYINYNDDORROEFFRFTNGKIV 327

Db 270 LVMPELSTGLARYLAFHPVDGLVKTLALITLQFLGYIIFRGANGCKNRFSPNPND--- 326

QY 328 WGRAPKIVASTYTTTSGETKTSLLLTSGWNGIARHHEHYVPETLSAEFTWVPALFDNFIAY 387

Dd 327 ----PKLKLKFIQTRGK---LLISGWCGRNHINIFGDMIMAMWCLPAGFGSPIDY 379

07	308	FIVFIFLLELFDRANKDDRCKSNICKIWKLYCE	421
0b	380	FVVAYFEGVLTVHRNARDNHKCRVVKVSGEDFEKKK	413

probable C-14 stereo] reductase (EC 1.1.-.-) : No more data

C;Species: Neurospora crassa
C;Date: 13-Jan-1995 #sequence-revision 13-Jan-1995 #text-change 17-Mar-2000

R; Papavinasundaram, K.G.; Kasbekar, D.P.
Submitted to the EMRI Data Library March 1994
CJAccession: S441/0

A;Reference number: S44170
A;Accession: S44170

A:status: preliminary
A:Molecule type: DNA
A:Position: 1,400,000,000

A:Cross-references: EMBL:X77955; NID:g473245; PID:g473246
C:Genetics:

A: Introns: 26/2
C: Superfamily: yeast probable C-14 sterol reductase

Query Match 18.3%: Score 473.5: DB 2: length 490:
 o/nof/ncrse: carboxylactide, transmembrane protein

Best Local Similarity 30.9%; Pred. No. 2.5e-32;
Matches 133; Conservative 61; Mismatches 151; Indels 85; Gaps 18;

48 W-ENGUGLINIMPRPTLIAMKIIFCYGAFEAIIQLLPGRVEGPISPACNRPYKANG 106

Db 75 WPDNGVFGFLS-W-----SATLWTL--GYVALSVQYRFLPGHHVEGTLELSTGGRLLKINA 128

QY 107 LAAYEYTLATYIG-----LMMFGLFNPALIVYDHLGELFSALLIGSFIFCVLLYIK 156

Db 129 FNSAMCTLTLAAGTIAOGAEPFVTF-----ISDNFNOITISANITLFAFALAFVYVR 181

QY 157 G-HVAPSSD-----SSGSGNLIIDFYWGMELYPRIQ---KSPDIFVTNCRGMSMW 205

Db 182 SDYKFRGNKDMQOLAAGVYTGSLIDFYIGRELNRITPLIGQVDIKEFPMRGLLGM 241

QY 206 AVLAVTYCIKOYEINGKVSMSLVNTILMLVYTRKFFWMEAGYWNMTMDIAHGRGFYICW 265

Db 242 IILNCAFIKQYRXLGYVDSILITLTAIOAFYFEDGIWEPALVLTMTDTTGDFGFMSEF 301

QY 266 GCLVWPSPYITSPGMLVNHPELGT--QLAI-YILVAGILCIYINQCDROGRFRTN 322

Db 302 GDVWVWFMYSTQTRLVSHPOOLAAGLAVGAVLAAGYSIFRLS---NSQKNF-RTN 357

QY 323 GKCLVWGRAPSKIVASYTTTSGEKT-SLLTSGWMLARHHPYVPELISAFWTVP--- 378

Db 358 PE-----DPYKHLTYL-----QTKGSRLLITSGWMLARHNYLGDMLQSPYSLPTGI 407

QY 379 -----ALFDN-----FLATYVYFLULLFLDRAKDDRCR 409

Db 408 AGYQILSAGSNAPGATMTLDGREVVQGEARGWGIYFTYPIILYFAILLIHRDLRDERKS 467

QY 410 SKYGYWKLY 419

Db 468 KKYGDWERY 477

RESULT 7

S30769

Probable C-14 sterol reductase (EC 1.1.-.-) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein N0593; protein YNL280C

C:Species: Saccharomyces cerevisiae

C:Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 20-Jun-2000

C:Accession: S30769; S63254

R:Lorenz, R.T.

submitted to the EMBL Data Library, November 1992

A:Description: Cloning, sequencing, and disruption of the gene encoding sterol C-14 red

A:Reference number: S30769

A:Accession: S30769

A:Molecule type: DNA

A:Residues: 1-438 <LOR>

A:Cross-references: EMBL:M99419; NID:g171142; PID:g171143

R:Jessen, F.; Dubois, E.; Vierendeels, F.; Scherens, B.; Pierard, A.; Glansdorff, N.

submitted to the Protein Sequence Database, April 1996

A:Reference number: S63254

A:Accession: S63254

A:Molecule type: DNA

A:Residues: 1-438 <MES>

A:Cross-references: EMBL:271556; NID:g1302350; PID:g1302351; MIPS:YNL280C

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:ERG24

A:Cross-references: SGD:S0005224; MIPS:YNL280C

A:Map position: 14L

C:Superfamily: yeast probable C-14 sterol reductase

C:Keywords: oxidoreductase; transmembrane protein

F:17-33/Domain: transmembrane #status predicted <TM1>

F:74-90/Domain: transmembrane #status predicted <TM2>

F:109-125/Domain: transmembrane #status predicted <TM3>

F:145-161/Domain: transmembrane #status predicted <TM4>

F:247-263/Domain: transmembrane #status predicted <TM5>

F:312-328/Domain: transmembrane #status predicted <TM6>

Query Match 16.4%; Score 424.5; DB 2: Length 438;
Best local similarity 29.7%; Pred. No. 3.2e-28;
Matches 130; Conservative 74; Mismatches 160; Indels 73; Gaps 20;

QY 23 PPFVILLWYTHQDGSVYQTFGFF-----WENGVO-----GLINIMPRPILLIANK 68

Db 28 PVFTIIL-NQMRPDYFIK---GFQNFIDIVELW-NGIKPLRYLGNRELM----- 73

QY 69 IIFC-YGAFAEIIQLLLPGKRVBGPISPAQNPVYKANKLAAYFTLATYIGIMWFGIF 126

Db 74 TVYCLWGLIL-AVIDVILIPKRVKQVQLRDGSKLSYKINKI-AMSTVLVLAIRKMLTD 131

QY 127 N-PAIY-----DHGEIFSAIIFGSFI-----FCVLLYIK---GHVAPSSSDSGSG 170

Db 132 GQPELDQYIENHVSCLITISLPSFLATYCYAASFPLIFKKNNGKREKILALGNSG 191

QY 171 NLIDFYGMELYPRICKSPDIAKVTNCRGMSMAVLAATYCIKOYEINGKVSMSLVN 230

Db 192 NIIDWETIGRELNRILG-PIDIKMFSELRRGMILMLINLSCHHHHLKTKXINDALVYL 250

QY 231 TILMLVYTRKFFWMEAGYWNMTMDIAHGRGFYICWGLVWVWPSPYITSPGMLVNHPELG 290

Db 251 NFDGFIYFDGVLEBESVLTMMDTTDFGFMALFGLSLPFTYISQARTLSVSEYELG 310

QY 291 TOLAYILVAGILCI-----YINQCDROGRFRTNKGKLVWGRAPSKIVASYTTSGE 345

Db 311 -----WVKVVGIIAMFLGFHIFHSANKQSEFRQ--GKL-----ENLKSIOFTRKG- 354

QY 346 TKTSLLTSGWMLARHHPYVPELISAFWTVPALFNPFLATYVYFLULLFLDRAKRD 405

Db 355 TK-----LLCDGWMKSOHINFGWMLISLWCLATWFTQPLTYYSIXFATLLHROORDE 411

QY 406 DRCRSKYGYWKLYCEK 422

Db 412 HKCRKTYGENWEYERK 428

RESULT 8

T18681

hypothetical protein B0250.9 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18681

R:Lloyd, C.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19005

A:Accession: T18681

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-697 <WIL>

A:Cross-references: EMBL:281453; PIDN:CAB03797.1; GSPDB:GN00023; CESP:B0250.9

A:Experimental source: clone B0250

C:Genetics:

A:Gene: CESP:B0250.9

A:Map position: 5

A:Introns: 211/3; 281/3; 318/3; 372/1; 436/1; 490/1; 618/1

Query Match 16.1%; Score 418.5; DB 2: Length 697;

Best local similarity 29.3%; Pred. No. 1.7e-27;

Matches 122; Conservative 76; Mismatches 200; Indels 19; Gaps 9;

QY 10 VTYASMSLAFCEPPEVILLWYTHQDGS---SVTQPFGEWENGVQGLINIMPRPILLI 65

Db 286 VSAQWVALLIIVPPAPFFLFYSIHGTGLFVPTIFALFLRF-PLVLCQVPVW---DTV 341

QY 66 AMKIIFCGAEFALLIQLLPKRVBGPISPAQNPVYKANKLAAYFTLATYIGIMWFGI 125

Db 342 AWKFSAVNCAIQLIFWVWLPDQAL-WVSSAGDO-MREVNSFEFCILITCLLYVIGASAGV 399

QY 126 FNPALVYDHLGEISALIFGSFIFCVLLYIKGHVAPSSSDSGSGNLIIDFYWGMELYPR 185

Db 400 YRGDIIVYHFSNII--LIFA--IFAVLIW-----AALATYHFGVITVTSERWFEIENHPK 451

QY 186 IGSFEDIKVTNCRGMSMAVLAATYCIKOYEINGKVSMSLVNTILMLVYTRKFFWME 245

Db 452 I-LDIDLSFIRTRFTYIWPFLVISAANYFKHTYGGQISTVSLVCLSSVOLLYIQFHMNE 510

QY 246 AGYNTMDIAHGRGFYICWGLVWVWPSPYITSPGMLVNHPELGTOLATYILVAGILCI 305

Db 511 DLFLNSLDSKRCDFEYIMADFNVLGPIITYSPTIIVAINRSVVISNCLFCAVAIGSM 570
 QY 306 YINVDORROEFRRRTNCKLWGRAPSKIVASYTTTSGEFTSLILSGWGLARHPHY 365
 Db 571 VETACDKQKYEFRKSKTLLAVGVDAFFISAKYRTDSGDANTLLSGHWGCRHPNY 630
 QY 366 VPEILSAFFWVPALFDNFALFYVIFLTLILFRAKRDDRCRSKYKWKLYCEK 422
 Db 631 ASEAITFAAFSAFOGFSTIAHISFLYFLFLVARAFDENRCLIKGYQWAOYCSK 687

RESULT 9

nuclear envelope membrane protein-like - Arabidopsis thaliana
 T47551
 N:Alternate names: protein F8J2.110
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T47551
 R:Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, M.; Mayer, K.F.X.
 Submitted to the Protein Sequence Database, April 2000
 A:Reference number: 224458
 A:Accession: T47551
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-317 <NYA>
 A:Cross-references: EMBL:AL132969
 A:Experimental source: cultivar Columbia; BAC clone F8J2
 C:Genetics:
 A:Map position: 3
 A:Insertions: 12/3; 52/1; 75/3; 94/3; 125/2; 141/2; 176/3; 202/2; 242/2; 267/2
 A:Note: F8J2.110

Query Match 14.3%; Score 371.5; DB 2; Length 317;
 Best local similarity 28.7%; Pred. No. 6.9e-24;
 Matches 107; Conservative 68; Mismatches 107; Indels 91; Gaps 16;

QY 62 PTLIAKIIIFCYGAFAIQLLLPGKREVEGPISPAGNRPYKANGLAAYVTLATYGLW 121
 Db 8 PSLGSYVLYVEFYVYLAAGELIPGKVIKRGILSDSGQLRRCGLLA-LILVALILGIC 66
 QY 122 -WEIFNPALVYDHLGEIFLSALIGSFICYL---LYIKGHVAPSSSDSGS-----CG 170
 Db 67 AKLIVPELVYADRLGELLSA---TFICVLYTLATYVGR---SSSNKSGSLKPHVSG 119
 QY 171 NLIDFWMGMLYPRICKSPDIKVTNCRFGMSMAVLAATYCTCKQKEINQXSDSLVN 230
 Db 120 NLVNDWFGIOLNPOF-MSIDLKA-----GMMGMLILNLSILAKSVQ-DGSLQSOMILY 171
 QY 231 TILMLVYVTFEFWMEAGYVWNTMDIAHNRGFGYICWGLVWVPSVYTSFGMYLVNHPYELG 290
 Db 172 QIFC-----AGMW-----LLANKYE-- 166
 QY 291 TQLALIVLVAGILCIITYNY---DCDQROEFRRRTNCKLWGRAPSKIVASYTTTSGEFT 346
 Db 187 --LIVPAIVNCLVFLIGYVWFRGANKQKHIFK-NPKRTIWGKRP-----VVVGGK- 235
 QY 347 KTSLLLSGMMGLARHPHYVEILSAFFWVPALFDNFALFYVIFLTLILFRAKRDD 406
 Db 236 ----LLVSGVWGLARHCNLYLADMLALSLFPCGISSPVFYFYTLILILIMRERDEV 291
 QY 407 RCRSKYGRWKLY 419
 Db 292 RCAEKYEIMAEY 304

RESULT 10

probable transposon protein ERG4 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein G3725; hypothetical protein YGL012w; hypothetical
 C:Species: Saccharomyces cerevisiae
 C:Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 21-Jul-2000
 C:Accession: S64014; S15042; S31559

R:Hebling, U.; Hofmann, B.; Delius, H.
 Submitted to the Protein Sequence Database, May 1996
 A:Reference number: S64003
 A:Accession: S64014
 A:Molecule type: DNA
 A:Residues: 1-473 <HEB>
 A:Cross-references: EMBL:472534; NID:g1322468; PID:g1322469; MIPS:YGL012w
 A:Experimental source: strain S288C
 R:Chen, W.; Capleau, E.; Balzi, E.; Goffeau, A.
 Yeast 7, 305-308, 1991

A:Title: The YGL022 gene encodes a putative transport protein.
 A:Reference number: S15042; MUID:91353085; PMID:1882555
 A:Accession: S15042
 A:Molecule type: DNA
 A:Residues: 1-365, 'V', 367-473 <YEA>
 A:Cross-references: GB:S57891; NID:9234324; PID:AA19615.1; PID:9234325
 A:Experimental source: strain IL125-2B
 R:Chen, W.; Balzi, E.; Capleau, E.; Choder, M.; Goffeau, A.
 Yeast 7, 287-299, 1991
 A:Title: The DNA sequencing of the 17 kb HindIII fragment spanning the LEU1 and ATE1
 ntrolling pleiotropic drug resistance.
 A:Reference number: S15040; MUID:91353083; PMID:1882553
 A:Accession: S31559
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-365, 'V', 367-473 <CHE>
 A:Cross-references: GB:S58126; NID:9234321; PID:AA13895.1; PID:94261595
 C:Genetics:
 A:Gene: SGD:ERG4
 A:Cross-references: SGD:S0002980; MIPS:YGL012w
 A:Map position: 7L
 C:Superfamily: yeast probable C-14 sterol reductase

C:Keywords: transmembrane protein
 F:46-62/Domain: transmembrane #status predicted <TM1>
 F:103-119/Domain: transmembrane #status predicted <TM2>
 F:153-169/Domain: transmembrane #status predicted <TM3>
 F:175-191/Domain: transmembrane #status predicted <TM4>
 F:330-346/Domain: transmembrane #status predicted <TM5>
 F:424-440/Domain: transmembrane #status predicted <TM6>

Query Match 14.3%; Score 371; DB 2; Length 473;
 Best local similarity 26.4%; Pred. No. 1.2e-23;
 Matches 115; Conservative 71; Mismatches 202; Indels 48; Gaps 15;

QY 15 MSLAFCPPVLLMYTWHODGSYT-OTRGEFW-----ENGVOGLINIMPR 61
 Db 46 VIGMLIGFPLMLYWMICAEFYHGKVALPKAGESWMEITKHLUYOLVLENGI----- 96
 QY 62 PTLIAKIIIFCYGAFAIQLLLPGKREVEG-PISP-AGNRPYKANGLAAYVTLATYGL 119
 Db 97 PEKYDWTIFLTFWVNPQIIYTYLPGIWTGQPLSHLKGQLYFCNAMWTLVYTTTLVLV 156
 QY 120 LWMFGIFNPALVYDHLGEIFLSALIGSFICYLTYKGVHAPSSSDSGCGLIIDFYWG 179
 Db 157 LHFTNLFRLVYIIDRGRIMTCAIISGFASIIYL-NTLFTSHDYHRMTGHNHLDVDFMG 215
 QY 180 MELYPRICKSPDIKVTNCRFGMSMAVLAATYCTCKQKEINQXSDSLVNITILMLVYT 239
 Db 216 APLNPRWG-IIDLMKEFEVRLPMFTLYFTTLGACLKQWETGYVYVPLQGVWLAHMLVN 274
 QY 240 KFEWMEAGYVWNTMDIAHNRGFGYICWGLVWVPSVYTSFGMYLVNHPYELG-----TOLA 294
 Db 275 ACAKGEELVPTWDMAYEKFGMLIFMNLAGVPTTYCHCTILVLYHDSBYMSTLYNVS 334
 QY 295 IYILVAGILCIITYND-CDROEER-----RTNCKLWGRAPSKIVAS--YTTTSGE 345
 Db 335 LYVV--LLCAYYFFDTANAOKNAKFKQMSGDTKRTPF--LPYQLIKNPKYVWTS-- 387
 QY 346 TTSLLLSGMMGLARHPHYVEILSAFFWVPALFDNFALFYVIFLTLILFRAKRDD 405
 Db 388 -NGSYLLIDGWTTLAKKIHITADWTQSLWALSCGNSVFPFVFLVYLIRAFRDQ 446
 QY 406 DRCRSKYGRWKLYCE 421

Db 447 AKCKRKYKMDYCK 462

||:|||||:|:

RESULT 11

A43765 stsl+ protein - fission yeast (Schizosaccharomyces pombe)

C:Species: Schizosaccharomyces pombe

C>Date: 18-Nov-1992 #sequence_revision 18-Nov-1992 #text_change 01-Dec-2000

C:Accession: A43765; T38121

R:Shimanuki, M.; Goebel, M.; Yanagida, M.; Toda, T.

Mol. Biol. Cell 3, 263-273, 1992

A:Title: Fission stsl(+) gene encodes a protein similar to the chicken lamin B

A:Reference number: A43765; MUID:92329994; PMID:1320960

A:Accession: A43765

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-453 <SH1>

A:Cross-references: GB:X63549; NID:95108; PIDN:CAA45113.1; PID:95109

R:Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, August 1996

A:Reference number: Z21771

A:Accession: T38121

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-411, 'C', 413-453 <CON>

A:Cross-references: EMBL:Z98600; PIDN:CA811256.1; GSPDB:GN00066; SPDB:SPAC20G4.07C

A:Experimental source: strain 972h-; cosmid c20G4

C:Genetics:

A:Gene: SPDB:SPAC20G4.07C

A:Map position: 1

C:Superfamily: yeast probable C-14 sterol reductase

C:Keywords: transmembrane protein

Query Match 14.0%; Score 363.5; DB 2; Length 453;

Best Local Similarity 26.8%; Pred. No. 4.9e-23;

Matches 117; Conservative 69; Mismatches 204; Indels 47; Gaps 12;

Qy 16 LSLAFCPPVILLMTVMYHODGSVOTGCF--WENGVOGL--INIMPRPTLAWKI 69
 Db 20 LAIMTGPCMLMYLWMAKSKRNDQFTRKESFTAGQNFRTIGHYIGANPTRAFLV 79
 Qy 70 IFCYGAFAELLQLLPQKRYEG-PISPAGN-RPVYKANGLAAYVTLATYLGIMWGFIFN 127
 Db 80 FMSFCIAQAVMYLPLGVRTQGLPKHRNNEBRLPYLCMAIWSRYTIVLAVLHTVHPV 139
 Qy 128 PAIVYDHLGEIFSAIFGSIIFCVLXY-----KGHAPSSSDSGSGNLIIDF 176
 Db 140 ITTFIDMFGPLMSVAITTAATVCTFVLYTGLTFGRDLFDPKPH-----RUSGNPIYDA 191
 Qy 177 YMGELAYPRIGKSFIDIKVFNCRFGMMNAVL--AVTYCIKOYEINGKVSMSLVNTIL 233
 Db 192 FMGACLNPRIGKLLDFKMFPEVR---IPWILFFISVGAANRKYETGVYSPVLFVCG 248
 Qy 234 MLVYVTFEWMWEGYNTMDIAHDSGFYICWGLVWDSVYTSPOMYLVNHPVEL--G 290
 Db 249 HYLVAANASGEOLIVPTMDMAYEKGFMLEFNMAAGVFPYTSCHLLYLFSDPSVYNNMS 308
 Qy 291 TOLAIYLVAGIICITVINYCDRODERF---TNGKCLWGRAPSKIVAST--TTS 343
 Db 309 TQYTTGTIVYLLCCYYIFDTGNGCKNHFNRQIYGEVHRKTFPQDLMLIKNPTFIRCAN 368
 Qy 344 GEFTSLTLTSGWMLGARHPHYVEILISAFWTVPALFDNFLAYFVIFLTLTLLFDRAR 403
 Db 369 GGI---LTLGMYRARKIHTYADFPQSLSMALITGFQSPPLFYFPSPFFVVLVHRSR 424
 Qy 404 DDDCRSKYKGYKWC 420
 Db 425 DIKKCKAKYAGDFEYC 441

RESULT 12

S14138

cytochrome-c oxidase (EC 1.9.3.1) chain I - sugar beet mitochondrion
 C:Species: mitochondrion Beta vulgaris var. altissima (sugar beet)
 C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 23-Jul-1999
 C:Accession: S14138
 R:Sendra, M.; Harada, T.; Mikami, T.; Sugiyama, M.; Kinoshita, T.
 Curr. Genet. 19, 175-181, 1991
 A:Title: Genomic organization and sequence analysis of the cytochrome oxidase subunit
 A:Reference number: S14138; MUID:91330331; PMID:1651175
 A:Accession: S14138
 A>Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-524 <SEN>
 A:Cross-references: GB:X57693; GB:S47702; NID:911258; PIDN:CAA40874.1; PID:911259
 C:Genetics:
 A:Gene: coxi
 A:Genome: mitochondrion
 C:Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
 C:Keywords: chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane
 F:12-459/Domain: cytochrome-c oxidase chain I homology <CO1>
 F:64,380/Binding site: heme a iron (His) (axial ligands) #status predicted
 F:243,292,293/Binding site: copper (His) #status predicted
 F:243-247/Cross-link: 1'-histidyl-3'-lysine (His-Tyr) #status predicted
 F:247/Binding site: oxygen (Tyr) #status predicted
 F:370/Binding site: magnesium (His) (shared with chain II) #status predicted
 F:378/Binding site: heme a3 iron (His) (axial ligand) #status predicted

Query Match 4.6%; Score 120.5; DB 2; Length 524;

Best Local Similarity 20.4%; Pred. No. 0.022;

Matches 110; Conservative 56; Mismatches 169; Indels 205; Gaps 28;

Qy 64 LIAW-----KIIFCYGAFAEI-----IQLLPGRKRVGSPISPAQNPVYK 103
 Db 4 LYRMFLSTNNHMDIGTYIFGAIAGVMTGCTSVLIRHLAGPQGIIG-----GNHQLVN 58
 Qy 104 A-----NGLAIFVYATYATLGLW--WFG---TFNPAYVYDHLGIFSAIFGSIIFCVLL 153
 Db 59 VLITAHAFIMTFEWMFMIGFGFNWFPILIGADMAFPRLNNISFWLPPS---LTL 114
 Qy 154 YIKGHVAPSSSDSGSCGLIIDFPWGMELYPRI-----GKSPDIKVF----- 195
 Db 115 LLSALVEVSGGTC-----W--TVYPLSGITSHSGAVDLAIFSLHLSGVSSIL 162
 Qy 196 -----TNCRFGMMNAVLAVTYCIKOYEINGKVSMSLVNTILMLVYV 238
 Db 163 GSINFTITTFNMRGPGMHRRLPFWMSVLVTAFL-----LLSLPVLATITMLTFD 215
 Qy 239 TKFWMWEGYNTMDIAHDSGFYICWGLVW--PSY--TSPGMVNVHPVE----- 288
 Db 216 RNF-----NTTFEPDAGGDDPLLYOHLWFGHPEVYLLLPFGILSHIVSTESGK 267
 Qy 289 -----LGTOLA-IYTLVAGIL-----CIYINYDDRODERF-----TNGKCLWVG 329
 Db 268 PVEGYLGMVYAMISIGVIGFLVMAHMTVGLDWD-IRAYTAATMILAYPTGKIISW- 325
 Qy 330 RAPSRIVASVYTTSGERTSLLTSGW-----WGLARHP 363
 Db 326 -----IATMWSGISQYKTPMLFAVGFIPLFTVAGIAGIYLVANGDLIALHDITYVAHF 379
 Qy 364 HYV-----PELISAF-FWTVPALDNLNPLAYVYVIFLTL 397
 Db 380 HYLISMGAVALFAGFYWVGKIFGRYTPETLGOIHFI--TFEGVNLTFPPMFLGLSG 437
 Qy 398 FDRARDDDRSKYKGYKWKLYCEKSNTPREFIDCNEWCSSHLLTLTIRLESSKDR 457
 Db 438 MPRRIID-----YPDAYAGMNLSSGYSIISVIGIC-FFVYVYI--TSSGKNK 484

RESULT 13

S65346

cytochrome-c oxidase (EC 1.9.3.1) chain I - tomato mitochondrion

C:Species: mitochondrion Lycopersicon esculentum (tomato)
 C>Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000

Page 7

Oy	154 YIKGVHAPSSSDSGSCGNLLIDFYWMGMELYPRY-----CKSPDIKVF-----
Dd	115 LLTSALVEVGSQT- - - - -W--FVYPPLSGITSHSAGAVDLAIFSLHSQVSIL 162
Oy	196 -----TNCFGMMSMAVLATYYCIKOTELNGAKXSDSMYLNTIMLVVV 238
Dd	163 GSINFTTTTFNNRGPGMTNHRLPFLFWSVLTYAFLL-----LLTPLVALGITMLTLTD 215
Oy	239 TKFFWMEAGYWNTMDIADHDGFYCICMGCLVNV---PSVY--TSPGMVLVNHPV----- 288
Dd	216 RNF-----NTTFPDPAAGGDPLLQHLEMFEGHPEVYLIIILEFGISIHYSPTFS GK 267
Oy	289 ----LGTOLA-IYILLVAIGIL-----CIVINYDCROROEFRP-----TNCKGLWWG 329
Dd	268 PVFGYLGHWVMYMISMIGVLGLTWAMHMFTVGLDVD-TRAYFTAAMTIAYVPGIKIETSW- 325
Oy	330 RAPSKVASYTTHSETRTSLLTISGW-----WGIAHHF 363
Dd	326 ----IATMMGGSIQYKTPMLFAVGEFTFLTGTGLTVLANSGDIALDHDTYVAAHF 379
Oy	364 HYV-----PELLSN-FEVTVALPDFNLAEYVFIPLTL 397
Dd	360 HVIYSKGAVPALFACEYYYWGKIEGRITYPETTGQIHEWI--TFGVNMTEFPPIHFLISG 437
Oy	398 FDRANRDDRCRSKYKKWKLYCEKSNTGPSREFIDCNVCSSHPLTLTRLETSSKDR 457
Dd	438 MPRRIIPD-----YPDVAAGMNALSSTGYISVYGICC-PFVYVTI--TLSGKNK 484
RESULT 14	
S14139	
Cytochrome c oxidase (EC 1.9.3.1) chain I - radish mitochondrion	
C:Species:	Mitochondrion Raphanus sativus (radish)
C>Date:	16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 23-Jul-1999
C:Accession:	S14139
R:Makaroff,	C.A.; Apel, T.J.; Palmer, J.D.
Curr. Genet.	19, 183-190, 1991
A>Title:	The role of coxi-associated repeated sequences in plant mitochondrial DNA re
A:Reference number:	S14139; MUID:9133033Z; PMID:1651176
A:Accession:	S14139
A>Status:	not compared with conceptual translation
A:Molecule type:	DNA
A:Residues:	1..527 <MARK>
A:Cross-references:	GB:X57692; NID:g297415; PIDB:CA440873.1; PDB:g297416
C:Gene:	coxI
A:Genome:	mitochondrion
C:Superfamily:	Cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C:Keywords:	chromoprotein; copper; electron transfer; heme; iron; magnesium; membrane transmembrane protein
F:1/2-459/Domains:	Cytochrome-c oxidase chain I homology <COO>
E:64_380/Binding site:	Heme A iron (His) (axial ligands) #status predicted
E:243_292_293/Binding site:	Copper (His) #status predicted
E:243-247/Cross-link:	I-Histidyl-3'-tyrosine (His-Tyr) #status predicted
F:247/Binding site:	Oxygen (Tyr) #status predicted
F:370/Binding site:	magnesium (His) (shared with chain II) #status predicted
F:378/Binding site:	Heme a3 iron (His) (axial ligand) #status predicted
Query Match	Score 115.5; DB 2; Length 527;
Best Local Similarity	20.2%; Pred. No. 0.058;
Matches 109; Conservative 56; Mismatches 170; Indels 205; Gaps 28;	
Oy	LIAW-----KIIFYCGAFPAEI-----LOLLPKRKVRGPISPAGNRPVVK 103
Dd	4 LVRLPFENNHEDITLFIFIRCALINGWCTCRSYLRBELARPGQIIIG-----GNHOLYN 58
Oy	104 A----NGLAAFVTLATTYGLW--WFG---IFNPDAIVDHLAGIFSALIIFGFCVL 153
Dd	59 VLTAAHLFMLEIFFVMPAMDIMGCFGNWFVPLIGAPDMAFPLANNISFWLPPS---LLL 114
Oy	154 YIKGVHAPSSSDSGSCGNLLIDFYWMGMELYPRI-----GKSPDIVF----- 195
Dd	115 LLSALLAVEVGSQT- - - - -W--TVYPPLSGITSHSAGAVDLAIFSLHSQVSIL 162

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QY 196 -----TNCREGMSMAVLAVTYCIKQKINGKSDSLVNTILMLVYV 238
Db 163 GSINFTTTTNNKRGPGMTNHRLLPLFWASVLYTAFL-----LISLPLACATMLLTD 215
QY 239 TRFWWAGYVNTMDIAHNRGEYICWGLVWY---PSVY--TSPGMYLVNHPV----- 288
Db 216 RNF-----NTFFPDPAAGGDPILYQHLFWFPGHPEVYILILPGGIIISHIVTFSGK 267
QY 289 -----LGTOLA-IYILVAGIL-----CIYINDCROROBEFR-----TNGCLYWG 329
Db 268 PVFGYLGMYAMISIGVLGEFLWAMHMTVGLVD--TRAYFLAAMTIAVPGIIFGSM- 325
QY 330 RAPSRIVASVTTTSGEETKSLTSGM-----WGLARHF 363
Db 326 -----IATWGGSIQYKIPMLFANGFIFLFTIGITGIVLANSGLDIALHDTYVVAHF 379
QY 364 HVY-----PELISAF-FWTVPALFDFNLAYFYVIELTLL 397
Db 380 HYLSMGAVFALFAGFYVWVGKIFGRTPETLQIHFWI--TEFGVNLFFPMHFLGLSG 437
QY 398 FDRAKDDDRCKSKYKGYKLYCEKSNIGSFREDICNVCSSHLLITLITLSSKDR 457
Db 438 MPERRIPD-----YPDAYAGWALSSFGSISVWGIC--FFVYVYI--TLSSGNK 484

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RESULT 15

S67084 probable membrane protein YOR192c - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein O4759

C:Species: *Saccharomyces cerevisiae*

C>Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002

C:Accession: S67084

R: Hughes, B.; Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66685

A:Accession: S67084

A:Molecule type: DNA

A:Residues: 1-599 <HUG>

A:Cross-references: EMBL:Z75100; NID:q1420458; PID:q1420459; GSPDB:GN00015; MIPS:YOR192C

A:Experimental source: strain S288C

C:Genetics:

A:Gene: MIPS:YOR192C

A:Cross-references: SGD:S0005718

A:Map position: 15R

C:Superfamily: uracil transport protein

C:Keywords: transmembrane protein

F:78-94/Domain: transmembrane #status predicted <TM1>

F:116-132/Domain: transmembrane #status predicted <TM2>

F:174-190/Domain: transmembrane #status predicted <TM3>

F:199-215/Domain: transmembrane #status predicted <TM4>

F:280-296/Domain: transmembrane #status predicted <TM5>

F:398-414/Domain: transmembrane #status predicted <TM6>

F:447-463/Domain: transmembrane #status predicted <TM7>

F:485-501/Domain: transmembrane #status predicted <TM8>

Query Match 4.2%; Score 108; DB 2; Length 599;

Best Local Similarity 18.4%; Pred. No. 0.29;

Matches 86; Conservative 70; Mismatches 172; Indels 140; Gaps 24;

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QY 9 IVTVASMLSLAFCPPEVILM-YTMVHODGSVTO-----TEGFFW 48
Db 131 IVYYSNAWLGGCLVNNILDSWHLHLPLNTLSSKVAMTKELLGFIIFHILTAFCYFM 190
QY 49 ENGVOGLINIMPRPTLIAMKIIFCYGAFAIIOI---LLPKRVESGPISPAGNRPYKAN 105
Db 191 KPYHMYIILWS-----CVGTFEALMGVITYITKSAHGVGDLFTSHSTVTGSK 239
QY 106 GLAAYFTLATYGLMWFQIFNPAIV---YDHLGE---IFSALFSGFICVLLIYIKG 157
Db 240 KAMAWYTTIS---YWGSVSPGCTINQSDFSRFGSSNCAIMVGTIVALLIPATLIPVFG 294
QY 158 HVAPSSSDSGSCNLLIDFYW-GMELYPRIGKSFIDIKVFNCRFGMSMAVLAVTYCIKQ 216

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Db 295 IIGAS-----ACEKLYGQTFWMPMDI-----EDNNLFTNYSAGARA-ATFFCGGCFYW 341
QY 217 YEINGKVSDSLAVNTIILMYVTKFEFWWEGYNNNTMDIAH-----DRGIFY---ICM 265
Db 342 SQISYTTISN-----CGFASGMDLACLPRKYVDIKRGALFAACVSM 381
QY 266 GCLVWVPSVYTSFGMYLVNHPVELGTLATYIIVAGILCIYINVDNR--ORQEFRRN 322
Db 382 ACLPW--NFYNSSSEFL-----VMSDFGVMTPIITVMI---CDNFLIRKQYSVTN 429
QY 323 GKCLVWRADSKIVASYTTTSGEETKSLTSGM-----WGLARHFIYPEIL 370
Db 430 AFVL-----KGEYFTKGVNMRIV--AWVCGMADLPGLIWEVNNDYFHTGTII 477
QY 371 SAFFWTYPALFDNFLAYFYIETLLFD--RAKRDDECRSKYGY 415
Db 478 NEFYGD---SFSPLISFFYWGICLLEPRKITVKKHD--KQYGA 519

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Search completed: January 14, 2003, 14:17:52
Job time : 26 secs

1	2280	87.9	430	1	US-08-601-043-2	Sequence 2, Appl1
2	2280	87.9	430	2	US-08-331-047-2	Sequence 2, Appl1
3	2280	87.9	430	2	US-08-783-202-2	Sequence 2, Appl1
4	2280	87.9	430	4	US-09-443-041A-31	Sequence 31, Appl1
5	1981	76.4	430	4	US-09-443-041A-18	Sequence 18, Appl1
6	1976.5	76.2	450	4	US-09-443-041A-22	Sequence 22, Appl1
7	1960	75.6	432	4	US-09-443-041A-20	Sequence 20, Appl1
8	559	21.5	419	1	US-08-439-131A-3	Sequence 3, Appl1
9	559	21.5	419	1	US-08-440-674-2	Sequence 2, Appl1
10	554	21.4	134	4	US-09-443-041A-8	Sequence 8, Appl1
11	544.5	21.0	161	4	US-09-443-041A-6	Sequence 6, Appl1
12	499.5	19.3	418	4	US-09-442-653-7	Sequence 7, Appl1
13	418.5	16.1	438	1	US-08-439-131A-2	Sequence 2, Appl1
14	418.5	16.1	438	1	US-08-440-674-5	Sequence 5, Appl1
15	368	14.2	473	1	US-08-439-131A-4	Sequence 4, Appl1
16	368	14.2	473	1	US-08-440-674-3	Sequence 3, Appl1
17	354.5	13.7	453	1	US-08-439-131A-5	Sequence 5, Appl1
18	354.5	13.7	453	1	US-08-440-674-4	Sequence 4, Appl1
19	253	9.8	74	4	US-09-443-041A-2	Sequence 2, Appl1
20	249	9.6	67	4	US-09-443-041A-4	Sequence 4, Appl1
21	216.5	8.3	145	4	US-09-342-653-4	Sequence 4, Appl1
22	161	6.2	81	4	US-09-342-653-6	Sequence 6, Appl1
23	105	4.0	68	4	US-09-442-653-2	Sequence 2, Appl1
24	97	3.7	352	4	US-09-576-160B-3	Sequence 3, Appl1
25	92.5	3.6	352	4	US-09-576-160B-1	Sequence 1, Appl1
26	92	3.5	451	4	US-09-134-001C-4420	Sequence 4420, Appl1
27	91.5	3.5	444	4	US-08-482-746-15	Sequence 15, Appl1

45	81.5	3.1	252	4	US-09-134-001C-4109	Sequence 4109, App1
44	82.5	3.2	1095	4	US-09-112-09C-15	Sequence 778, App1
43	82.5	3.2	1095	4	US-09-112-09C-15	Sequence 778, App1
42	82.5	3.2	467	4	US-09-134-001C-4020	Sequence 3020, App1
41	83	3.2	3010	4	US-09-014-416-3	Sequence 3, App1
40	83	3.2	530	4	US-09-134-001C-5510	Sequence 4510, App1
39	84	3.2	800	4	US-09-134-001C-5655	Sequence 5655, App1
38	84.5	3.3	309	5	PCF-UD93 -08548-56	Sequence 56, App1
37	84.5	3.3	309	5	US-08-118-270-56	Sequence 56, App1
36	85	3.3	446	4	US-09-633-696-11	Sequence 11, App1
35	85	3.3	446	2	US-08-672-814D-11	Sequence 11, App1
34	87	3.4	446	3	US-08-833-035A-15	Sequence 15, App1
33	87	3.4	446	2	US-08-833-610-5	Sequence 5, App1
32	88	3.4	448	4	US-08-934-254-5	Sequence 5, App1
31	88	3.4	448	1	US-08-789-93C-5	Sequence 5, App1
30	88	3.4	448	1	US-08-966-779-5	Sequence 5, App1
29	89.5	3.5	352	4	US-09-576-160B-2	Sequence 2, App1
28	91.5	3.5	618	4	US-08-595-553A-2	Sequence 2, App1

ALIGNMENTS

```

1  RESULT 1
2  US-08-601-435-2
3  : Sequence 2, Application US/08601435
4  : Patent No. 5759801
5  : GENERAL INFORMATION:
6  : APPLICANT:
7  : TITLE OF INVENTION: DNA sequence coding for a protein
8  : TITLE OF INVENTION: of A. thaliana having a delta-5,7 sterol, delta-7
9  : TITLE OF INVENTION: reductase activity, delta7-Red protein, production
10 : TITLE OF INVENTION: process, strains of transformed yeasts, uses.
11 : NUMBER OF SEQUENCES: 31

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/601,435
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9501723
FILING DATE: 15-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9506517
FILING DATE: 01-JUN-1995
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-601-435-2

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Query Match	87.98;	Score 2280;	DB 1;	Length 430;
Best Local Similarity	98.88;	Pred. No. 2.7e-226;		
Matches 417;	Conservative	1;	Mismatches 2;	Indels 2;
				Gaps 1

QY	1	MAETVSP ¹ IVT ² YAS ³ MS ⁴ LS ⁵ LAC ⁶ CP ⁷ EV ⁸ LL ⁹ WT ¹⁰ Y ¹¹ W ¹² H ¹³ O ¹⁴ G ¹⁵ S ¹⁶ T ¹⁷ O ¹⁸ P ¹⁹ FG ²⁰ F ²¹ W ²² MS ²³ V ²⁴ Q ²⁵ GI ²⁶ NI ²⁷ NP	60
Db	1	MAETVSP ¹ IVT ² YAS ³ MS ⁴ LS ⁵ LAC ⁶ CP ⁷ EV ⁸ LL ⁹ WT ¹⁰ Y ¹¹ W ¹² H ¹³ O ¹⁴ G ¹⁵ S ¹⁶ T ¹⁷ O ¹⁸ P ¹⁹ FG ²⁰ F ²¹ W ²² MS ²³ V ²⁴ Q ²⁵ GI ²⁶ NI ²⁷ NP	60
QY	61	RPL ¹ L ² W ³ K ⁴ I ⁵ IF ⁶ YGA ⁷ FEA ⁸ LI ⁹ DL ¹⁰ LL ¹¹ PK ¹² R ¹³ VE ¹⁴ SP ¹⁵ IS ¹⁶ PA ¹⁷ NP ¹⁸ RY ¹⁹ KA ²⁰ NI ²¹ AA ²² P ²³ TA ²⁴ TY ²⁵ GL	120
Db	61	RPL ¹ L ² W ³ K ⁴ I ⁵ IF ⁶ YGA ⁷ FEA ⁸ LI ⁹ DL ¹⁰ LL ¹¹ PK ¹² R ¹³ VE ¹⁴ SP ¹⁵ IS ¹⁶ PA ¹⁷ NP ¹⁸ RY ¹⁹ KA ²⁰ NI ²¹ AA ²² P ²³ TA ²⁴ TY ²⁵ GL	120
QY	61	RPL ¹ L ² W ³ K ⁴ I ⁵ IF ⁶ YGA ⁷ FEA ⁸ LI ⁹ DL ¹⁰ LL ¹¹ PK ¹² R ¹³ VE ¹⁴ SP ¹⁵ IS ¹⁶ PA ¹⁷ NP ¹⁸ RY ¹⁹ KA ²⁰ NI ²¹ AA ²² P ²³ TA ²⁴ TY ²⁵ GL	120
Db	61	RPL ¹ L ² W ³ K ⁴ I ⁵ IF ⁶ YGA ⁷ FEA ⁸ LI ⁹ DL ¹⁰ LL ¹¹ PK ¹² R ¹³ VE ¹⁴ SP ¹⁵ IS ¹⁶ PA ¹⁷ NP ¹⁸ RY ¹⁹ KA ²⁰ NI ²¹ AA ²² P ²³ TA ²⁴ TY ²⁵ GL	120
QY	121	WM ¹ GF ² IN ³ PA ⁴ IV ⁵ YD ⁶ HL ⁷ GE ⁸ IF ⁹ SA ¹⁰ LI ¹¹ FG ¹² ST ¹³ IF ¹⁴ CV ¹⁵ LL ¹⁶ IK ¹⁷ GH ¹⁸ VA ¹⁹ PSS ²⁰ SD ²¹ GS ²² CN ²³ LI ²⁴ ID ²⁵ FT ²⁶ WG ²⁷ M	180
Db	121	WM ¹ GF ² IN ³ PA ⁴ IV ⁵ YD ⁶ HL ⁷ GE ⁸ IF ⁹ SA ¹⁰ LI ¹¹ FG ¹² ST ¹³ IF ¹⁴ CV ¹⁵ LL ¹⁶ IK ¹⁷ GH ¹⁸ VA ¹⁹ PSS ²⁰ SD ²¹ GS ²² CN ²³ LI ²⁴ ID ²⁵ FT ²⁶ WG ²⁷ M	180
QY	121	WM ¹ GF ² IN ³ PA ⁴ IV ⁵ YD ⁶ HL ⁷ GE ⁸ IF ⁹ SA ¹⁰ LI ¹¹ FG ¹² ST ¹³ IF ¹⁴ CV ¹⁵ LL ¹⁶ IK ¹⁷ GH ¹⁸ VA ¹⁹ PSS ²⁰ SD ²¹ GS ²² CN ²³ LI ²⁴ ID ²⁵ FT ²⁶ WG ²⁷ M	180
Db	121	WM ¹ GF ² IN ³ PA ⁴ IV ⁵ YD ⁶ HL ⁷ GE ⁸ IF ⁹ SA ¹⁰ LI ¹¹ FG ¹² ST ¹³ IF ¹⁴ CV ¹⁵ LL ¹⁶ IK ¹⁷ GH ¹⁸ VA ¹⁹ PSS ²⁰ SD ²¹ GS ²² CN ²³ LI ²⁴ ID ²⁵ FT ²⁶ WG ²⁷ M	180

QY 181 ELYPRIGKSEDIKVFETNCRFGMMSNAVLAVTYCIKOYEINGKVSMSLNTLMLVYTK 240
 DB 181 ELYPRIGKSEDIKVFETNCRFGMMSNAVLAVTYCIKOYEINGKVSMSLNTLMLVYTK 240
 QY 241 FFWMEAGYNTMTDIAHNRGCFYICWGLVWVPSVYSPGMYLVNHPVEIGTOLATYILVA 300
 DB 241 FFWMEAGYNTMTDIAHNRGCFYICWGLVWVPSVYSPGMYLVNHPVEIGTOLATYILVA 300
 QY 301 GILCTIYINCDROROEFRTNCKLWGRAPSKIVASVTTTSGETKTSLLTSGMWGLA 360
 DB 301 GILCTIYINCDROROEFRTNCKLWGRAPSKIVASVTTTSGETKTSLLTSGMWGLA 360
 QY 361 RHFHYVEILSAFHWTVPALEFNLAFYVIFLTLLEFDRAKRDDRCRSKYGYKWLXC 420
 DB 361 RHFHYVEILSAFHWTVPALEFNLAFYVIFLTLLEFDRAKRDDRCRSKYGYKWLXC 418
 QY 421 EK 422
 DB 419 EK 420

RESULT 2

US-08-931-047-2
 ; Sequence 2, Application US/08931047
 ; Patent No. 5965417
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: DNA sequence coding for a protein of
 ; TITLE OF INVENTION: A. thaliana having a delta-5,7 sterol,
 ; TITLE OF INVENTION: delta-7 reductase activity, delta-7-Red
 ; TITLE OF INVENTION: protein, production process, strains
 ; NUMBER OF SEQUENCES: 31
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/931,047
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 9501723
 ; FILING DATE: 15-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 9506517
 ; FILING DATE: 01-JUN-1995
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 430 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-931-047-2

Query Match 87.9%; Score 2280; DB 2; Length 430;
 Best Local Similarity 98.8%; Pred. No. 2.7e-226;
 Matches 417; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAETVHSPIVTVASMLSLAFCEPPVILLMTWVHODGSVYOTGFGEWENGVOGLINIMP 60
 DB 1 MAETVHSPIVTVASMLSLAFCEPPVILLMTWVHODGSVYOTGFGEWENGVOGLINIMP 60
 QY 61 RPTLIAMKIIIFCYGAFAEAILIOLLPGKRVESPISPAGNRPYKANGLAAYFVTLATYLG 120
 DB 61 RPTLIAMKIIIFCYGAFAEAILIOLLPGKRVESPISPAGNRPYKANGLAAYFVTLATYLG 120
 QY 121 WMFGIFNPAIYVDHIGELIFSLIFGSEIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180
 DB 121 WMFGIFNPAIYVDHIGELIFSLIFGSEIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180

QY 181 ELYPRIGKSEDIKVFETNCRFGMMSNAVLAVTYCIKOYEINGKVSMSLNTLMLVYTK 240
 DB 181 ELYPRIGKSEDIKVFETNCRFGMMSNAVLAVTYCIKOYEINGKVSMSLNTLMLVYTK 240
 QY 241 FFWMEAGYNTMTDIAHNRGCFYICWGLVWVPSVYSPGMYLVNHPVEIGTOLATYILVA 300
 DB 241 FFWMEAGYNTMTDIAHNRGCFYICWGLVWVPSVYSPGMYLVNHPVEIGTOLATYILVA 300
 QY 301 GILCTIYINCDROROEFRTNCKLWGRAPSKIVASVTTTSGETKTSLLTSGMWGLA 360
 DB 301 GILCTIYINCDROROEFRTNCKLWGRAPSKIVASVTTTSGETKTSLLTSGMWGLA 360
 QY 361 RHFHYVEILSAFHWTVPALEFNLAFYVIFLTLLEFDRAKRDDRCRSKYGYKWLXC 420
 DB 361 RHFHYVEILSAFHWTVPALEFNLAFYVIFLTLLEFDRAKRDDRCRSKYGYKWLXC 418
 QY 421 EK 422
 DB 419 EK 420

RESULT 3

US-08-783-202-2
 ; Sequence 2, Application US/08783202
 ; Patent No. 5989881
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: DNA sequence coding for a protein of A.
 ; TITLE OF INVENTION: thaliana having a delta-5,7 sterol, delta-7 reductase
 ; TITLE OF INVENTION: activity, delta-7-Red protein, production process, strains
 ; NUMBER OF SEQUENCES: 31
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: IBM PC compatible
 ; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/783,202
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 9501723
 ; FILING DATE: 15-FEB-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 9506517
 ; FILING DATE: 01-JUN-1995
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 430 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-783-202-2

Query Match 87.9%; Score 2280; DB 2; Length 430;
 Best Local Similarity 98.8%; Pred. No. 2.7e-226;
 Matches 417; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAETVHSPIVTVASMLSLAFCEPPVILLMTWVHODGSVYOTGFGEWENGVOGLINIMP 60
 DB 1 MAETVHSPIVTVASMLSLAFCEPPVILLMTWVHODGSVYOTGFGEWENGVOGLINIMP 60
 QY 61 RPTLIAMKIIIFCYGAFAEAILIOLLPGKRVESPISPAGNRPYKANGLAAYFVTLATYLG 120
 DB 61 RPTLIAMKIIIFCYGAFAEAILIOLLPGKRVESPISPAGNRPYKANGLAAYFVTLATYLG 120
 QY 121 WMFGIFNPAIYVDHIGELIFSLIFGSEIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180
 DB 121 WMFGIFNPAIYVDHIGELIFSLIFGSEIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180
 QY 181 ELYPRIGKSEDIKVFETNCRFGMMSNAVLAVTYCIKOYEINGKVSMSLNTLMLVYTK 240
 DB 181 ELYPRIGKSEDIKVFETNCRFGMMSNAVLAVTYCIKOYEINGKVSMSLNTLMLVYTK 240

Db 181 ELVPRICKSDIKVTCNCRGMSMAVLAVYCIKQYEINGKVSMSLVNTIIMLVYTK 240
 QY 241 FFWMEAGYWNMTMDIAHNRGGEYICMGCLVWVPSYTSRGMVLVNHPELGTOLAIYTLVA 300
 Db 241 FFWMEAGYWNMTMDIAHNRGGEYICMGCLVWVPSYTSRGMVLVNHPELGTOLAIYTLVA 300
 QY 301 GILCIYINVDCCRORGFERRTNGKCLVWGRAPSKIVASYTTSGEYTSLLTSGMWGLA 360
 Db 301 GILCIYIKYDCDRORGFERRTNGKCLVWGRAPSKIVASYTTSGEYTSLLTSGMWGLA 360
 QY 361 RHHYVEILISAFFWTVPALFDNLAIFYIETLLLFDRAKRDDCRSKYKWKLYC 420
 Db 361 RHHYVEILISAFFWTVPALFDNLAIFYY -LTLLLFDRAKRDDCRSKYKWKLYC 418
 QY 421 EK 422
 Db 419 EK 420

RESULT 4
 US-09-443-041A-31
 ; Sequence 31, Application US/09443041A
 ; Patent No. 6465717
 ; GENERAL INFORMATION:
 ; APPLICANT: Farnodu, Omolayo O.
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Shen, Jennie
 ; TITLE OF INVENTION: Sterol Metabolism Enzymes
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/443,041A
 ; CURRENT FILING DATE: 1999-11-18
 ; PRIOR APPLICATION NUMBER: 60/109,283
 ; PRIOR FILING DATE: 1998-11-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 31
 ; LENGTH: 430
 ; TYPE: PRF
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-443-041A-31

Query Match 87.9%; Score 2280; DB 4; Length 430;
 Best Local Similarity 98.8%; Pred. No. 2,7e-226;
 Matches 417; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAEIVHSPIYTYASMSLAFCEPPEVILLMTYVHODGSVTQTFGEFWENGVOGLINIMP 60
 Db 1 MAEIVHSPIYTYASMSLAFCEPPEVILLMTYVHODGSVTQTFGEFWENGVOGLINIMP 60
 QY 61 RPTLIAMKIIFCYGAFFAIILQLLPGKRVEGPISPAENRPRVYKANGIAAFVTLATYGL 120
 Db 61 RPTLIAMKIIFCYGAFFAIILQLLPGKRVEGPISPAENRPRVYKANGIAAFVTLATYGL 120
 QY 121 WMEGIFNPALVYHDLGEIFSAIFGSEIFCVLLYIKGHVAPSSSDSGSCNLIIDFYMG 180
 Db 121 WMEGIFNPALVYHDLGEIFSAIFGSEIFCVLLYIKGHVAPSSSDSGSCNLIIDFYMG 180
 QY 181 ELVPRICKSDIKVTCNCRGMSMAVLAVYCIKQYEINGKVSMSLVNTIIMLVYTK 240
 Db 181 ELVPRICKSDIKVTCNCRGMSMAVLAVYCIKQYEINGKVSMSLVNTIIMLVYTK 240
 QY 241 FFWMEAGYWNMTMDIAHNRGGEYICMGCLVWVPSYTSRGMVLVNHPELGTOLAIYTLVA 300
 Db 241 FFWMEAGYWNMTMDIAHNRGGEYICMGCLVWVPSYTSRGMVLVNHPELGTOLAIYTLVA 300
 QY 301 GILCIYINVDCCRORGFERRTNGKCLVWGRAPSKIVASYTTSGEYTSLLTSGMWGLA 360
 Db 301 GILCIYIKYDCDRORGFERRTNGKCLVWGRAPSKIVASYTTSGEYTSLLTSGMWGLA 360
 QY 361 RHHYVEILISAFFWTVPALFDNLAIFYIETLLLFDRAKRDDCRSKYKWKLYC 420
 Db 361 RHHYVEILISAFFWTVPALFDNLAIFYY -LTLLLFDRAKRDDCRSKYKWKLYC 418

QY 421 EK 422
 Db 419 EK 420

RESULT 5
 US-09-443-041A-18
 ; Sequence 18, Application US/09443041A
 ; Patent No. 6465717
 ; GENERAL INFORMATION:
 ; APPLICANT: Farnodu, Omolayo O.
 ; APPLICANT: Orozco, Buddy
 ; APPLICANT: Rafalski, Antoni
 ; APPLICANT: Shen, Jennie
 ; TITLE OF INVENTION: Sterol Metabolism Enzymes
 ; FILE REFERENCE:
 ; CURRENT APPLICATION NUMBER: US/09/443,041A
 ; CURRENT FILING DATE: 1999-11-18
 ; PRIOR APPLICATION NUMBER: 60/109,283
 ; PRIOR FILING DATE: 1998-11-20
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 18
 ; LENGTH: 430
 ; TYPE: PRF
 ; ORGANISM: Oryza sativa
 ; US-09-443-041A-18

Query Match 76.4%; Score 1981; DB 4; Length 430;
 Best Local Similarity 83.3%; Pred. No. 1.6e-195;
 Matches 350; Conservative 34; Mismatches 36; Indels 0; Gaps 0;

QY 3 ETVHSPYTYASMSLAFCEPPEVILLMTYVHODGSVTQTFGEFWENGVOGLINIMP 62
 Db 1 KTVHSAIYTYASMSLAFCEPPEVILLMTYVHODGSVTQTFGEFWENGVOGLINIMP 60
 QY 63 TLIAMKIIFCYGAFFAIILQLLPGKRVEGPISPAENRPRVYKANGIAAFVTLATYGL 122
 Db 61 TMAAMKIIFCYGAFFAIILQLLPGKRVEGPISPAENRPRVYKANGIAAFVTLATYGL 120
 QY 123 FGIENPAIYVHDLGEIFSAIFGSEIFCVLLYIKGHVAPSSSDSGSCNLIIDFYMG 182
 Db 121 FGIENPAIYVHDLGEIFSAIFGSEIFCVLLYIKGHVAPSSSDSGSCNLIIDFYMG 180
 QY 183 YPRICKSDIKVTCNCRGMSMAVLAVYCIKQYEINGKVSMSLVNTIIMLVYTK 242
 Db 181 YPRICKSDIKVTCNCRGMSMAVLAVYCIKQYEINGKVSMSLVNTIIMLVYTK 240
 QY 243 WMEAGYWNMTMDIAHNRGGEYICMGCLVWVPSYTSRGMVLVNHPELGTOLAIYTLVA 302
 Db 241 WMEAGYWNMTMDIAHNRGGEYICMGCLVWVPSYTSRGMVLVNHPELGTOLAIYTLVA 300
 QY 303 LCIYINVDCCRORGFERRTNGKCLVWGRAPSKIVASYTTSGEYTSLLTSGMWGLA 362
 Db 301 LCIYINVDCCRORGFERRTNGKCLVWGRAPSKIVASYTTSGEYTSLLTSGMWGLA 360
 QY 363 RHHYVEILISAFFWTVPALFDNLAIFYIETLLLFDRAKRDDCRSKYKWKLYC 422
 Db 361 RHHYVEILISAFFWTVPALFDNLAIFYY -LTLLLFDRAKRDDCRSKYKWKLYC 420

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Query Match	76.2%;	Score 1976.5;	DB 4,	Length 450;
Best Local Similarity	83.6%;	Pred. No. 4.9e-195;		
Matches 351;	Conservative 33;	Mismatches 35;	Indels 1;	Gaps 1.

[illegible]

```

RESULT 7
US-09-443-041A-20
Sequence 20, Application US/09443041A
Patent No. 6465117
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Orozco, Buddy
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennie
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/443,041A
CURRENT FILING DATE: 1999-11-18
PRIOR APPLICATION NUMBER: 60/109,283
PRIOR FILING DATE: 1998-11-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 432
TYPE: PRT
ORGANISM: Glycine max
US-09-443-041A-20

```

Query Match	75.6%;	Score 1960;	DB 4;	Length 433;
Best Local Similarity	83.6%;	Pred. No. 2.3e-133;		
Matches 353;	Conservative 28;	Mismatches 41;	Indels 0;	Gaps 0

D0	1	MGATVHSP	ELVTYASV	ISLTL	CLCPFV	LLIWT	MTIADG	SVSETH	YKQNG	LOGLH	TWP	60	
QY	61	REP	LAMK	ILFCY	GA	FEA	ILLO	LLP	GR	KB	EB	SP	120
D0	61	T	PR	ACK	IL	IA	YA	FEA	AL	LL	P	GT	120
QY	121	WM	GJ	NP	AI	YV	DH	GL	GE	LS	AL	IG	180
D0	121	WM	GJ	NP	AI	YV	DH	GL	GE	LS	AL	IG	180
QY	181	EL	P	R	G	K	S	F	D	I	K	V	240
D0	181	EL	P	R	G	K	S	F	D	I	K	V	240
QY	241	F	M	W	E	A	G	Y	N	T	M	D	300
D0	241	F	M	W	E	A	G	Y	N	T	M	D	300
QY	301	G	I	L	C	I	Y	I	N	D	C	R	360
D0	301	G	I	L	C	I	Y	I	N	D	C	R	360
QY	361	R	H	E	H	Y	P	E	L	I	S	A	420
D0	361	R	H	E	H	Y	P	E	L	I	S	A	420
QY	421	E	K	422									
D0	421	E	K	422									

RESULT 8
 US-08-439-131A-3
 : Sequence 3, Application US/08439131A
 : Patent No. 5512472
 : GENERAL INFORMATION:
 : APPLICANT: Lai, Margaret H. K.
 : APPLICANT: Bard, Martin
 : APPLICANT: Kirsch, Donald R.
 : TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
 : Patent No. 5512472
 : TITLE OF INVENTION: Reductase
 : NUMBER OF SEQUENCES: 5
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: American Cyanamid Company
 : STREET: One Cyanamid Plaza
 : CITY: Wayne
 : STATE: New Jersey
 : COUNTRY: U.S.A.
 : ZIP: 07470
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/439,131A
 : FILING DATE: 11-MAY-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/107,347
 : FILING DATE: 16-AUG-1993
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Gordon, Alan M.
 : REGISTRATION NUMBER: 30,637
 : REFERENCE/DOCKET NUMBER: 854-012 (32,141)
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 201-831-3244
 : TELEFAX: 201-831-3305
 : INFORMATION FOR SEQ ID NO: 3:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 419 amino acids

```

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PUBLICATION INFORMATION:
AUTHORS: Worman, H. J.
AUTHORS: Evans, C. D.
AUTHORS: Blobel, G.
TITLE: The Lamin B Receptor of the Nuclear Envelope
JOURNAL: J. Cell Biol.
VOLUME: 111
PAGES: 1535-1542
DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO: 3: FROM 190 TO 608
US-08-439-131A-3

Query Match
Best Local Similarity 21.5%; Score 559; DB 1; Length 419;
Matches 137; Conservative 62; Mismatches 178; Indels 40; Gaps 11;

QY 18 LLAFCPPFVLLMYTMVHODGSVTQTF-----GFWENGVOGLINIMPRPTLAKKIIF 71
DB 21 MMEFLPAIVLYLVLMCKODPSLMNFPPLPALESIMETKVFVFLM-----FF 70
QY 72 CYGAFAEAILQLLLPGKRVEG-PISPAGNRPVYKANGLAAYVTATYGLMWFGLFNPAT 130
DB 71 ----FQALFYLLPIGKRVVEGLPLSNP-RKPQYRNGFYAFLTAATQTLTYFQ-FELHY 124
QY 131 VYDHGGEISALIFGSEIFCVLLYIKGHVAPSS--SDSGSCGNLIDYWGMELYPRIG 188
DB 125 LYDHFEVQFAVSAAFSMAISLYIRSLKAPBEDLAPGNSGYLVYNEFTEHLPRIG- 183
QY 189 SPDIKVTNCRFGMSMAVLAATVYCICKOYEINGKVSDSM---LVNTILMYVYTKFEME 245
DB 184 SFDIKYFCERLPGIGWVYINLMLAEKIHNSMPSLSMILVNS-FQLLYVVDALMNE 242
QY 246 AGYWNMTDIAHNRGGEFYICWGLVWPVSVYSPGMVLVNHPELGTOLAIYILVAGILCI 305
DB 243 EAVLTMTDITHDGFEMFLAFGLVWVPVYSLQAFYIVGHPIAISMPVAAITLINCIGY 302
QY 306 YINYDCDRQROEFRRTNGKCLVWGAPSKIVASYTTTSGETKTSLLTSGWGLARHFIY 365
DB 303 YIFRSANSQKNNFRN-----PADPKLSYLKVIPTATGKGLVTVGMGFEVRHPNY 352
QY 366 VPEILSAFETVPALEFNDLAFYVIFLTLDFRAKRODDRCRSKYGKWKLYCEK 422
DB 353 LGDITMALANSLPCGFNHLPIFYIYITCLLVHREARDEHCKKRYGLAMERYCOR 409

RESULT 9
US-08-440-674-2
Sequence 2, Application US/08440674
Patent No. 5525496
GENERAL INFORMATION:
APPLICANT: Margaret H. Lai
TITLE OF INVENTION: A DNA Sequence Encoding Sterol
Patent No. 5525496
TITLE OF INVENTION: 14
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESS: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 MB diskette
COMPUTER: IBM PC
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,674
FILING DATE: May 15, 1995
CLASSIFICATION: 536
PUBLICATION INFORMATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,347
FILING DATE: August 16, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Alan M. Gordon
REGISTRATION NUMBER: 30637
REFERENCE/DOCKET NUMBER: 854-P0012 DIV (32,141)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-831-3244
TELEFAX: 201-831-3305
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 419 residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: polypeptide
FEATURE:
NAME/KEY: chicken
NAME/KEY: nuclear lamin B receptor
PUBLICATION INFORMATION:
AUTHORS: H. J. Worman, C. D. Evans, and G.
AUTHORS: Blobel
TITLE: (excerpt): The Lamin B Receptor of the
JOURNAL: Nuclear Envelope Inner Membrane
VOLUME: 111
PAGES: 1535-1542
PAGES: Sequence set out in Figure 5, page 1539
DATE: 1990
RELEVANT RESIDUES IN SEQ ID NO: 190 TO 608
US-08-440-674-2

Query Match
Best Local Similarity 21.5%; Score 559; DB 1; Length 419;
Matches 137; Conservative 62; Mismatches 178; Indels 40; Gaps 11;

QY 18 LLAFCPPFVLLMYTMVHODGSVTQTF-----GFWENGVOGLINIMPRPTLAKKIIF 71
DB 21 MMEFLPAIVLYLVLMCKODPSLMNFPPLPALESIMETKVFVFLM-----FF 70
QY 72 CYGAFAEAILQLLLPGKRVEG-PISPAGNRPVYKANGLAAYVTATYGLMWFGLFNPAT 130
DB 71 ----FQALFYLLPIGKRVVEGLPLSNP-RKPQYRNGFYAFLTAATQTLTYFQ-FELHY 124
QY 131 VYDHGGEISALIFGSEIFCVLLYIKGHVAPSS--SDSGSCGNLIDYWGMELYPRIG 188
DB 125 LYDHFEVQFAVSAAFSMAISLYIRSLKAPBEDLAPGNSGYLVYNEFTEHLPRIG- 183
QY 189 SPDIKVTNCRFGMSMAVLAATVYCICKOYEINGKVSDSM---LVNTILMYVYTKFEME 245
DB 184 SFDIKYFCERLPGIGWVYINLMLAEKIHNSMPSLSMILVNS-FQLLYVVDALMNE 242
QY 246 AGYWNMTDIAHNRGGEFYICWGLVWPVSVYSPGMVLVNHPELGTOLAIYILVAGILCI 305
DB 243 EAVLTMTDITHDGFEMFLAFGLVWVPVYSLQAFYIVGHPIAISMPVAAITLINCIGY 302
QY 306 YINYDCDRQROEFRRTNGKCLVWGAPSKIVASYTTTSGETKTSLLTSGWGLARHFIY 365
DB 303 YIFRSANSQKNNFRN-----PADPKLSYLKVIPTATGKGLVTVGMGFEVRHPNY 352
QY 366 VPEILSAFETVPALEFNDLAFYVIFLTLDFRAKRODDRCRSKYGKWKLYCEK 422
DB 353 LGDITMALANSLPCGFNHLPIFYIYITCLLVHREARDEHCKKRYGLAMERYCOR 409

RESULT 10

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US-09-443-041A-8
; Sequence 8, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 134
; TYPE: PRF
; ORGANISM: Trifolium aestivum
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (124)
; OTHER INFORMATION: ANY AMINO ACID
US-09-443-041A-8

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Query Match
Best Local Similarity 21.4%; Score 554; DB 4; Length 134;
Matches 101; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

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QY 4 TVHSPITVYASMSLAFCEPPEVILLMTWVHODGSVTQTFEPFEMNGVQGLINIMPRT 63
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 TVHSAVTVYTSMLALSLCPPEVILLMTWVHODGSVTQTFEHLRHDGEGKAIWPMPT 60
QY 64 LVMKTIIFCGAFEDLIQLLPGKRVGSPISPAENRPPYKANGLAAYFTLATYGLWVF 123
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 LVMKTIIFGGLFEAVLIQLLPGKRVGSPISPAENRPPYKANGLAAYFTLATYGLWVF 120
QY 124 GTFNPAIVYDHGE 137
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 121 GTFNPAIVYDHGE 134

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RESULT 11
US-09-443-041A-6
; Sequence 6, Application US/09443041A
; Patent No. 6465717
; GENERAL INFORMATION:
; APPLICANT: Farnodu, Omolayo O.
; APPLICANT: Orozco, Buddy
; APPLICANT: Rafalski, Antoni
; APPLICANT: Shen, Jennie
; TITLE OF INVENTION: Sterol Metabolism Enzymes
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/443,041A
; CURRENT FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 60/109,283
; PRIOR FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 161
; TYPE: PRF
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (77)
; OTHER INFORMATION: ANY AMINO ACID
; NAME/KEY: UNSURE
; LOCATION: (95)
; OTHER INFORMATION: ANY AMINO ACID
; NAME/KEY: UNSURE
; LOCATION: (102)

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; OTHER INFORMATION: ANY AMINO ACID
; NAME/KEY: UNSURE
; LOCATION: (157)
; OTHER INFORMATION: ANY AMINO ACID
; NAME/KEY: UNSURE
; LOCATION: (159)
; OTHER INFORMATION: ANY AMINO ACID
US-09-443-041A-6

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Query Match
Best Local Similarity 21.0%; Score 544.5; DB 4; Length 161;
Matches 105; Conservative 15; Mismatches 41; Indels 1; Gaps 1;

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QY 1 MAETVHSPITVYASMSLAFCEPPEVILLMTWVHODGSVTQTFEPFEMNGVQGLINIMP 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 MGATVHSPITVYASVISTLTCPEVILLMTWVHODGSVTQTFEHLRHDGEGKAIWPMPT 60
QY 61 RPTLIAMKTIIFCGAFEDLIQLLPGKRVGSPISPAENRPPYKANGLAAYFTLATYGL 120
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 TPTTACKTIIVAAFYAALQILLPGKRVGSPISPAENRPPYKANGLAAYFTLATYGL 119
QY 121 WMFGTFNPAIVYDHGEFSLIFGSPITFCVLYIKGHVAPS 162
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 120 WMFGTFNPAIVYDHGEFSLIFGSPITFCVLYIKGHVAPS 161

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RESULT 12
US-09-342-653-7
; Sequence 7, Application US/09342653
; Patent No. 6306632
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Chromatin Associated Proteins
; FILE REFERENCE: BB-1118
; CURRENT APPLICATION NUMBER: US/09/342,653
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,841
; EARLIER FILING DATE: July 14, 1998
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 418
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-342-653-7

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Query Match
Best Local Similarity 19.3%; Score 499.5; DB 4; Length 418;
Matches 123; Conservative 60; Mismatches 167; Indels 25; Gaps 8;

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QY 54 GLINWPRPTLIAMKTIIFCGAFEDLIQLLPGKRVGSPISPAENRPPYKANGLAAYFT 113
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 53 GLEVIMSPRALLW---LAWIGLQALYLPARKVABGQELKDKSRIRYPINGQALVLT 109
QY 114 LATYGLWVFIFNPAIVYDHGEFSLIF---GSFIFCVLLIRGHVAPS--SDSG 167
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 110 -ALLVGLG---MSAGLPGLAPPEMLPLAVATLTAFTFELFYMAQVAPASALAPGG 164
QY 168 SCGNLIIDFWGMELVPRIGKSPDIKVFYTNCRFGSMGMAVLAATYCYKQYEINGKSDSM 227
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 165 NSGNPIYDFLGRLEINPRI-CEFDKFKYCELRPGLIGVILNIALMLKKEALRSGPSLAM 223
QY 228 LVNTILMLVYVTKFFWVAGVWNTMDLAHDGSGYIOMGCLVWVPSVYTSQWLVNHPV 287
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 224 WLWNGFQLLVYGDALWBEAVLTTMDTHDGFMLAFGDAMPFTYSLOAQPLHLHPQ 283
QY 288 ELGTOLAIYIVAGILCIYINWCDROEFRRTNGACLVWGRAPSKIVASYTTSETK 347
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 284 PLGLPMASVICLINALIGYIRGANSQKNTFRKKNPSDPRVAG-----LETISTATRK- 336
QY 348 TSLLTSGMWGIARHFHYVPEILSAFWYVPALEFNDPLAVFYVFTLLLFDRAKRDDDR 407
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 14
 US-08-440-674-5
 Sequence 5, Application US/08440674
 Patent No. 5525496
 GENERAL INFORMATION:
 APPLICANT: Margaret H. Lai
 TITLE OF INVENTION: A DNA Sequence Encoding Sterol
 Patent No. 5525496
 TITLE OF INVENTION: 14
 NUMBER OF INVENTION: Reductase
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07470
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" 1.44 Mb diskette
 COMPUTER: IBM PC
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word Processor
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/440,674
 FILING DATE: May 15, 1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/107,347
 FILING DATE: August 16, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Alan M. Gordon
 REGISTRATION NUMBER: 30637
 REFERENCE/DOCKET NUMBER: 854-P0012 Div (32,141)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-831-3244
 TELEFAX: 201-831-3305
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 438 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE:
 DESCRIPTION: polypeptide
 FRAGMENT TYPE: entire sequence
 IMMEDIATE SOURCE: *Saccharomyces cerevisiae*
 IMMEDIATE SOURCE: clone
 FEATURE:
 OTHER INFORMATION: translated polypeptide of
 OTHER INFORMATION: sterol 14
 OTHER INFORMATION: reductase gene
 US-08-440-674-5

Matches 129; Conservative 74; Mismatches 161; Indels 73; Gaps 20;

QY 23 PPVILLMTYVHODGSVTQTFGFF-----WENGVO-----GLINIMPRPLIAMK 68
 DB 28 PVFTILL-NQMRPBYFIK---GFONEDIVELW-NGIKPLRYLGNBELW-----73
 QY 69 IIFC--YGAFEALLOLLPGKRVEGISPAGNRPYKANGLAAYVTLATYGLMWPFI 126
 DB 74 TVYCLWYGLI-LAVDYLIFGRWKGVLORDGSKLSIKINGI-AMSTLVLVLAIRKLT 131
 QY 127 N--PAIVY---DHLGEIFSLIFGSFI-----FCVLLYIK---GHVAPSSSDGSGC 170
 DB 132 GQLEPELOYIYENHVSCLISILFEPFLAYCYVASFIPLEFKKNGKREKILACGNSG 191
 QY 171 NLIIIDFYGMELYPRIKGFIDIKVFTNCRFGMSAVLAIVYICIOYELNGKVSMSLVN 230
 DB 192 NIIDWFIRELINPRLG-PLDIKMFSELRPGMLMLINLSCLHHHYLKTGKINDALV 250
 QY 231 TILMLVYTRKFFWMEAGYNTNDIAHGRGFYICWGCLVWPSVYTPSGMYLVNHPVELG 290
 DB 251 NISQGFYIFDGVINEGVLTMDITTDGFMALFGDLSLVFTYSLOARYLSTVSPVELG 310
 QY 291 TOLATYILVAGILCI-----YINDDROROEPRRTNGKCLWGRAPSKIYASVTTTSGE 345
 DB 311 -----WKKVVGILALIMFLGFHFHSANKQKSEPRQ--GKL-----ENLKSITKRG- 354
 QY 346 YKTSLLTSGWGLARHRYVPELISAFETVPALFDNLFATFYIELTLLEFRAKRD 405
 DB 355 TK---LLCGWMAKSOHINYFGDWLISLWCLATWFOPLTYVSYLSEFATLLHROORDE 411
 QY 406 DRCRKYKYKWLKCEK 422
 DB 412 HKCRKLYGENWEYERK 428

RESULT 15
 US-08-439-131A-4
 Sequence 4, Application US/08439131A
 Patent No. 5512472
 GENERAL INFORMATION:
 APPLICANT: Lai, Margaret H. K.
 APPLICANT: Bard, Martin
 APPLICANT: Kirsch, Donald R.
 TITLE OF INVENTION: A DNA Sequence Encoding Sterol Delta
 Patent No. 5512472
 TITLE OF INVENTION: Reductase
 NUMBER OF SEQUENCES: 5
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: American Cyanamid Company
 STREET: One Cyanamid Plaza
 CITY: Wayne
 STATE: New Jersey
 COUNTRY: U.S.A.
 ZIP: 07470
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/439,131A
 FILING DATE: 11-MAY-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/107,347
 FILING DATE: 16-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Gordon, Alan M.
 REGISTRATION NUMBER: 30,637
 REFERENCE/DOCKET NUMBER: 854-012 (32,141)
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-831-3244
 TELEFAX: 201-831-3305

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 473 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Saccharomyces cerevisiae
 PUBLICATON INFORMATION:
 AUTHORS: Chen, W
 AUTHORS: Capleaux, E.
 AUTHORS: Balzi, E.
 AUTHORS: Goffeau, A.
 TITLE: The YGL022 Gene Encodes a Putative Transport
 TITLE: Protein
 JOURNAL: Yeast
 VOLUME: 7
 PAGES: 305-308
 DATE: 1991

US-08-439-131A-4

Query Match 14.2%; Score 368; DB 1; Length 473;
 Best Local Similarity 26.3%; Pred. No. 2e-29;
 Matches 114; Conservative 73; Mismatches 203; Indels 44; Gaps 15;

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 QY 62 PTLIAMKIIFCYGAFEALLOLLPGKRVEG-PISP-AGNRPYKANGLAAYVTLATYLG 119
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 QY 120 LMWEGIFNPALVYDHLGEIFSALIFGSFICVLLYIKGHVAPSSSDGSGCNLIDFYWG 179
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Search completed: January 14, 2003, 14:18:15
 Job time : 19 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 14:13:05 ; Search time 41 Seconds
(without alignments)
1547.007 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	1340	51.7	253	21	AAW03539 Arabidopsis thaliana
7	1220	47.0	231	21	AAW03539 Arabidopsis thaliana
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ALIGNMENTS

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DE	Arabidopsis thaliana	protein fragment SPQ ID NO: 68171.	
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KW	Protein identification; signal transduction pathway; metabolic pathway;		
KW	hybridisation assay; genetic mapping; gene expression control; promoter;		
KW	termination sequence.		
XX	Arabidopsis thaliana		
OS	Arabidopsis thaliana		
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PD	06-SEP-2000.		
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PF	25-FEB-2000; 2000EP-0301439.		
XX	25-FEB-2000; 2000EP-0301439.		
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PR	16-APR-1999; 99US-0129845.		
PR	19-APR-1999; 99US-0130077.		

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Human polypeptide
Zea mays protein f
Gene 13 related pe
Protein LBR differ
Arabidopsis thaliana
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Arabidopsis thaliana
Arabidopsis C-14 s
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Pinus radiata ster
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 QY 361 RHFHYVPEILSAFWTVPALFDNFLAYFYVIFLTLFEDAKRDPDRCKSKYKWKLYC 420
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 DB 421 EK 422

RESULT 2

AAW03567
 ID AAW03567 standard; Protein; 430 AA.

AC AAW03567;

DT 09-APR-1997 (first entry)

DE Arabidopsis thaliana delta-5,7-sterol, delta7-reductase.

KX Delta-7Red: 7-dehydrocholesterol reductase; C7-unsaturated sterol;

KW pregnenolone; plant; delta-5,7 sterol, delta-7 reductase;

KW myastatin resistance.
 XX Arabidopsis thaliana.
 OS EP727489-A1.
 XX 21-AUG-1996.
 PD 14-FEB-1996; 96EP-0400301.
 PF 01-JUN-1995; 95FR-0006517.
 PR 15-FEB-1995; 95FR-0001723.
 XX (R0US) R0USSEL-UCLAF.
 PA Chenivesse X, Dupont C, Lecain E, Pompon D;
 DR WPI; 1996-372876/38.
 DR N-PSDB; AAT39358.
 XX Nucleic acid encoding delta-5,7 sterol delta-7 reductase - esp. of
 PT A.thaliana, for producing pregnenolone-synthesizing yeast.
 PS Claim 6; Page 47-49; 82pp; French.

CC A myastatin-resistant clone containing cDNA which encodes the
 CC delta-5,7 sterol, delta-7 reductase enzyme of Arabidopsis thaliana
 CC was isolated from a cDNA library in yeast strain FY1679. The major
 CC sterol of the untransformed yeast strain is ergosterol. RP-HPLC
 CC analysis showed that in one clone the ergosterol was replaced by
 CC two major sterols which did not absorb at 285 nm. The insert from
 CC this clone was subcloned to localise the enzyme coding region and
 CC the cDNA sequence was determined. The enzyme having the present
 CC sequence is designated delta-7Red and reduces C7-unsaturated sterols.
 CC In particular, it is useful in the production of pregnenolone.

SQ Sequence 430 AA;

Query Match 87.9%; Score 2280; DB 17; Length 430;
 Best Local Similarity 98.8%; Pred. No. 7.2e-215;
 Matches 417; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 1 MAETVHSPIVTVASMLSLAFCEPFFVILMTYTMVHODGSVYOTGFGEWNGVGLINIMP 60
 DB 1 MAETVHSPIVTVASMLSLAFCEPFFVILMTYTMVHODGSVYOTGFGEWNGVGLINIMP 60
 QY 61 RPTLIAMKIIIFCYGAFEAIIQLLLPGKRVEGPISPAGNRPVYKANGLAAYFVTLATYIGL 120
 DB 61 RPTLIAMKIIIFCYGAFEAIIQLLLPGKRVEGPISPAGNRPVYKANGLAAYFVTLATYIGL 120
 QY 121 WMFGIENPAIVYDHLGEIFSAIIFGSFIICVLLYIKGHVAPSSDSCGNIIDFYWGM 180
 DB 121 WMFGIENPAIVYDHLGEIFSAIIFGSFIICVLLYIKGHVAPSSDSCGNIIDFYWGM 180
 QY 181 ELYPRIGKSPDIKVFETNCRFGMSMAVLAIVYCIKOYEINGKVSMSLVNTIIMLVYVTK 240
 DB 181 ELYPRIGKSPDIKVFETNCRFGMSMAVLAIVYCIKOYEINGKVSMSLVNTIIMLVYVTK 240
 QY 241 FFWMEAGYWNMTMDIAHNRGFGFYICWGLVWPVSYSYTPGMVLVNHPELGTOLAIYIIVA 300
 DB 241 FFWMEAGYWNMTMDIAHNRGFGFYICWGLVWPVSYSYTPGMVLVNHPELGTOLAIYIIVA 300
 QY 301 GILCIYIINYDCDROREFRRTNGKCLVWGRAPSKIVASTYTTSGETKSLILTSGMWGLA 360
 DB 301 GILCIYIINYDCDROREFRRTNGKCLVWGRAPSKIVASTYTTSGETKSLILTSGMWGLA 360
 QY 361 RHFHYVPEILSAFWTVPALFDNFLAYFYVIFLTLFEDAKRDPDRCKSKYKWKLYC 420
 DB 361 RHFHYVPEILSAFWTVPALFDNFLAYFYV--LTLFLPRAKRDRCRCKYKWKLYC 418
 QY 421 EK 422
 DB 419 EK 420

RESULT 3
AAG53538
ID AAG53538 standard; Protein; 418 AA.
XX
AC AAG53538;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68172.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129645.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
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PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
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PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144335.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147712.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
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PR 13-AUG-1999; 99US-0148568.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.

PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149920.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157865.
PR 06-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
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PR 14-OCT-1999; 99US-0159329.
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PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161459.
PR 26-OCT-1999; 99US-0161460.
PR 26-OCT-1999; 99US-0161461.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161933.
PR 29-OCT-1999; 99US-0162142.

Query Match 86.4%; Score 2242; DB 21; Length 418;
Best Local Similarity 99.8%; Pred. No. 4.3e-215;
Matches 407; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 MSLSLAFCEPFVLLWMTYMHOGSGSYQTGTFWENGVOGLINWPRPLLIAKKIIFCG 74
DB 1 MSLSLAFCEPFVLLWMTYMHOGSVTQTFGFWENGVOGLINWPRPLLIAKKIIFCG 60
QY 75 AFPAIQLLLPGKRVCEPISPAKNRPYKANGLAAYFVLATYLGIMWGIENPAIVYDH 134
DB 61 AFPAIQLLLPGKRVCEPISPAKNRPYKANGLAAYFVLATYLGIMWGIENPAIVYDH 120
QY 135 LGEIFSALEFSEIFCVLLYIKGHVAPSSSDSGCNLLIIDFYGMELYPRIKGSFDIV 194

DB 121 LGEIFSALEFSEIFCVLLYIKGHVAPSSSDSGCNLLIIDFYGMELYPRIKGSFDIV 180
QY 195 FTNCRFGMMASAVLATYTIKQYEINGKYSDSLVTILMLVYTKFWEAGYNTMDI 254
DB 181 FTNCRFGMMASAVLATYTIKQYEINGKYSDSLVTILMLVYTKFWEAGYNTMDI 240
QY 255 AHDRCGEYICWGLWVPVSPGMYLVNHPVEIGTQATYILVAGLICITINDCRO 314
DB 241 AHDRCGEYICWGLWVPVSPGMYLVNHPVEIGTQATYILVAGLICITINDCRO 300
QY 315 ROEFFRTNGKCLWGRAPSKIVASYTTTSGTKTSLITSGMWGLARHPHYPEILSAF 374
DB 301 ROEFFRTNGKCLWGRAPSKIVASYTTTSGTKTSLITSGMWGLARHPHYPEILSAF 360
QY 375 WTVPALFDNPLAFYVIFLTLLFDPAKRDRCRSKRYGKYLCEK 422
DB 361 WTVPALFDNPLAFYVIFLTLLFDPAKRDRCRSKRYGKYLCEK 408

RESULT 4
AAG53539
ID AAG53539 standard; Protein; 400 AA.
XX AAG53539;
AC AAG53539;
XX 18-OCT-2000 (first entry)
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 68173.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68173.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX
XX EP1033405-A2.
PN 06-SEP-2000.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131444.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132485.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999;	99US-0136021.
PR 27-MAY-1999;	99US-0136392.
PR 28-MAY-1999;	99US-0136782.
PR 01-JUN-1999;	99US-0137222.
PR 03-JUN-1999;	99US-0137528.
PR 04-JUN-1999;	99US-0137502.
PR 07-JUN-1999;	99US-0137724.
PR 08-JUN-1999;	99US-0138094.
PR 10-JUN-1999;	99US-0138540.
PR 10-JUN-1999;	99US-0138847.
PR 14-JUN-1999;	99US-0139119.
PR 16-JUN-1999;	99US-0139452.
PR 17-JUN-1999;	99US-0139453.
PR 17-JUN-1999;	99US-0139454.
PR 18-JUN-1999;	99US-0139455.
PR 18-JUN-1999;	99US-0139456.
PR 18-JUN-1999;	99US-0139457.
PR 18-JUN-1999;	99US-0139458.
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PR 18-JUN-1999;	99US-0139460.
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PR 18-JUN-1999;	99US-0139462.
PR 18-JUN-1999;	99US-0139463.
PR 18-JUN-1999;	99US-0139750.
PR 18-JUN-1999;	99US-0139763.
PR 21-JUN-1999;	99US-0139817.
PR 22-JUN-1999;	99US-0139899.
PR 23-JUN-1999;	99US-0140353.
PR 23-JUN-1999;	99US-0140354.
PR 24-JUN-1999;	99US-0140695.
PR 28-JUN-1999;	99US-0140823.
PR 29-JUN-1999;	99US-0140991.
PR 30-JUN-1999;	99US-0141287.
PR 01-JUL-1999;	99US-0141842.
PR 02-JUL-1999;	99US-0142154.
PR 06-JUL-1999;	99US-0142055.
PR 08-JUL-1999;	99US-0142390.
PR 09-JUL-1999;	99US-0142820.
PR 12-JUL-1999;	99US-0142877.
PR 13-JUL-1999;	99US-0143542.
PR 14-JUL-1999;	99US-0143624.
PR 15-JUL-1999;	99US-0144005.
PR 16-JUL-1999;	99US-0144085.
PR 16-JUL-1999;	99US-0144086.
PR 19-JUL-1999;	99US-0144325.
PR 19-JUL-1999;	99US-0144331.
PR 19-JUL-1999;	99US-0144332.
PR 19-JUL-1999;	99US-0144333.
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PR 19-JUL-1999;	99US-0144335.
PR 20-JUL-1999;	99US-0144352.
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PR 20-JUL-1999;	99US-0144884.
PR 21-JUL-1999;	99US-0144814.
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PR 22-JUL-1999;	99US-0145085.
PR 22-JUL-1999;	99US-0145087.
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PR 27-JUL-1999;	99US-0145919.
PR 28-JUL-1999;	99US-0145951.
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PR 02-AUG-1999;	99US-0146588.
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PR 03-AUG-1999;	99US-0147038.
PR 04-AUG-1999;	99US-0147204.
PR 04-AUG-1999;	99US-0147302.
PR 05-AUG-1999;	99US-0147192.
PR 05-AUG-1999;	99US-0147260.
PR 06-AUG-1999;	99US-0147303.
PR 06-AUG-1999;	99US-0147416.
PR 09-AUG-1999;	99US-0147493.
PR 09-AUG-1999;	99US-0147935.
PR 10-AUG-1999;	99US-0148171.
PR 11-AUG-1999;	99US-0148319.
PR 12-AUG-1999;	99US-0148341.
PR 13-AUG-1999;	99US-0148365.
PR 13-AUG-1999;	99US-0148684.
PR 16-AUG-1999;	99US-0149368.
PR 17-AUG-1999;	99US-0149175.
PR 18-AUG-1999;	99US-0149426.
PR 20-AUG-1999;	99US-0149722.
PR 20-AUG-1999;	99US-0149723.
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PR 23-AUG-1999;	99US-0149930.
PR 25-AUG-1999;	99US-0150566.
PR 26-AUG-1999;	99US-0150884.
PR 27-AUG-1999;	99US-0151065.
PR 27-AUG-1999;	99US-0151066.
PR 27-AUG-1999;	99US-0151080.
PR 30-AUG-1999;	99US-0151303.
PR 31-AUG-1999;	99US-0151458.
PR 01-SEP-1999;	99US-0151930.
PR 07-SEP-1999;	99US-0152363.
PR 10-SEP-1999;	99US-0153070.
PR 13-SEP-1999;	99US-0153758.
PR 15-SEP-1999;	99US-0154018.
PR 16-SEP-1999;	99US-0154039.
PR 20-SEP-1999;	99US-0154779.
PR 22-SEP-1999;	99US-0155139.
PR 23-SEP-1999;	99US-0155486.
PR 24-SEP-1999;	99US-0155659.
PR 28-SEP-1999;	99US-0156458.
PR 29-SEP-1999;	99US-0156596.
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PR 05-OCT-1999;	99US-0157753.
PR 06-OCT-1999;	99US-0157865.
PR 07-OCT-1999;	99US-0158029.
PR 08-OCT-1999;	99US-0158232.
PR 12-OCT-1999;	99US-0158369.
PR 13-OCT-1999;	99US-0159283.
PR 13-OCT-1999;	99US-0159294.
PR 13-OCT-1999;	99US-0159295.
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PR 18-OCT-1999;	99US-0159584.
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PR 21-OCT-1999;	99US-0160767.
PR 21-OCT-1999;	99US-0160768.
PR 21-OCT-1999;	99US-0160770.
PR 21-OCT-1999;	99US-0160814.
PR 21-OCT-1999;	99US-0160815.
PR 22-OCT-1999;	99US-0160980.
PR 22-OCT-1999;	99US-0160981.
PR 22-OCT-1999;	99US-0160989.
PR 25-OCT-1999;	99US-0161404.
PR 25-OCT-1999;	99US-0161405.
PR 25-OCT-1999;	99US-0161406.
PR 26-OCT-1999;	99US-0161359.
PR 26-OCT-1999;	99US-0161360.
PR 26-OCT-1999;	99US-0161361.
PR 28-OCT-1999;	99US-0161920.
PR 28-OCT-1999;	99US-0161992.

PR 28-OCT-1999; 9905-0161993.
PR 29-OCT-1999; 9905-0162142.
Query Match 82.6%; Score 2143; DB 21; Length 400;
Best Local Similarity 99.7%; Pred. No. 3.1e-205;
Matches 389; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 33 MVHDDGAVTQTFEFGFWENGVOGLINIMPRPLIMKTIIFCGAFEAIIQILLPGKRVGP 92
Db 1 MVHDDGAVTQTFEFGFWENGVOGLINIMPRPLIMKTIIFCGAFEAIIQILLPGKRVGP 60
QY 93 ISPGNRPVYKANGLAAYFVTLATYLGIMWGFIPNALIVYDHLGEISALIFGSFICVL 152
Db 61 ISPGNRPVYKANGLAAYFVTLATYLGIMWGFIPNALIVYDHLGEISALIFGSFICVL 120
QY 153 LYIKGHVAPSSDSSGSGNLIIDFYNMELYPRIKGSFIDIKVFNCGFMSAVLAVTY 212
Db 121 LYIKGHVAPSSDSSGSGNLIIDFYNMELYPRIKGSFIDIKVFNCGFMSAVLAVTY 180
QY 213 CIRQYEINGKVSMSLVNTILMLVYVRFKFWMEAGYNNMTDIADRGCFYICMGCLVWP 272
Db 181 CIRQYEINGKVSMSLVNTILMLVYVRFKFWMEAGYNNMTDIADRGCFYICMGCLVWP 240
QY 273 SVYSPGMYLVNHPVEIGTQAIYILVAGILCIYINDCORQROEFRTNGKCLVWGRAP 332
Db 241 SVYSPGMYLVNHPVEIGTQAIYILVAGILCIYINDCORQROEFRTNGKCLVWGRAP 300
QY 333 SKIYASTTSGEFTKSTLLTSGMGLARHRYHYPETLSAFPTVPALEFNFLAYFVIF 392
Db 301 SKIYASTTSGEFTKSTLLTSGMGLARHRYHYPETLSAFPTVPALEFNFLAYFVIF 360
QY 393 LTLLFDRAKRDDRCRSKYKWKLYCEK 422
Db 361 LTLLFDRAKRDDRCRSKYKWKLYCEK 390
RESULT 5
ID AAG23597 standard; Protein; 376 AA.
AC AAG23597;
XX 17-OCT-2000 .(first entry)
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26964.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX
XX Arabidopsis thaliana.
OS
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126264.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
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PR 21-JUL-1999; 99US-0145086.
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 PR 23-AUG-1999; 99US-0149930.
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 PR 27-AUG-1999; 99US-0151080.
 PR 30-AUG-1999; 99US-0151303.
 PR 31-AUG-1999; 99US-0151330.
 PR 01-SEP-1999; 99US-0151930.
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 PR 10-SEP-1999; 99US-0153070.
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 PR 26-OCT-1999; 99US-0161359.
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 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 77.5%; Score 2011; DB 21; Length 376;
 Best Local Similarity 99.78; Pred. No. 4,4e-192; Mismatches 1; Indels 0; Gaps 0;
 Matches 365; Conservative 0;

OY 57 NIMPRPTLIANKIIFCYGAFAIILQLLPCKRVGSPISPAENRPFYKANGIAAFVTLAT 116
 DB 1 NIMPRPTLIANKIIFCYGAFAIILQLLPCKRVGSPISPAENRPFYKANGIAAFVTLAT 60
 OY 117 YLGLMVEGIFNPAIVYDHLGEISFALIFGSPICVLLYIKGHVAPSSDSGSGNLTIDF 176
 DB 61 YLGLMVEGIFNPAIVYDHLGEISFALIFGSPICVLLYIKGHVAPSSDSGSGNLTIDF 120
 OY 177 YMGELVPRIGKSPDIVETNCRFGMSMAVLAATYCIKOYEINIGKXSDSMLVNTILMV 236
 DB 121 YMGELVPRIGKSPDIVETNCRFGMSMAVLAATYCIKOYEINIGKXSDSMLVNTILMV 180
 OY 237 YVTKFVWWEAGYVNTMDIAHDSRGFYICWGLVWPVSYSYSPGMYLVNHVELETOLAIY 296
 DB 181 YVTKFVWWEAGYVNTMDIAHDSRGFYICWGLVWPVSYSYSPGMYLVNHVELETOLAIY 240
 OY 297 ILVAGILCTIYNTDODROREFRRTNGKCLWGAAPSKYASVTTTSGERTSILLTSGW 356
 DB 241 ILVAGILCTIYNTDODROREFRRTNGKCLWGAAPSKYASVTTTSGERTSILLTSGW 300
 OY 357 WGLARHFHYVPEIISAFFWTVPALEDNFLAFYVYIFITLLFDRAKDDRCRKYGYW 416
 DB 301 WGLARHFHYVPEIISAFFWTVPALEDNFLAFYVYIFITLLFDRAKDDRCRKYGYW 360
 OY 417 KLYCEK 422
 DB 361 KLYCEK 366

RESULT 6
 AAG23598
 ID AAG23598 standard; Protein; 253 AA.
 XX AAG23598;
 AC
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 26965.
 XX
 KW Protein identification: signal transduction pathway; metabolic pathway;
 KM hydrolisation assay; genetic mapping; gene expression control; promoter;
 XX termination sequence.
 OS Arabidopsis thaliana.
 XX
 PM EPI033405-A2.
 XX
 PD 06-SEP-2000.
 XX

PR 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 23-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
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PR 28-APR-1999; 99US-0130891.
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PR 03-JUN-1999; 99US-0137528.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151308.
PR 31-AUG-1999; 99US-0151383.
PR 01-SEP-1999; 99US-0151930.
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 PR 29-OCT-1999; 99US-0162142.

Query Match 51.7%; Score 1340; DB 21; Length 253;
 Best Local Similarity 99.6%; Pred. No. 2,6e-125;
 Matches 242; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 180 MELYPRIGKSFIDIKYFTNCRFGNMSWAVLAVTYCIKQYKINGKSDSMLVNTLMELVYVT 239
 DB 1 MELYPRIGKSFIDIKYFTNCRFGNMSWAVLAVTYCIKQYKINGKSDSMLVNTLMELVYVT 60
 QY 240 KFFWMEAGYWNMTMDLAHDGGRFICWGLVWPVSYYTSGMTLVNHPVBLGQLAIYIIV 299
 DB 61 KFFWMEAGYWNMTMDLAHDGGRFICWGLVWPVSYYTSGMTLVNHPVBLGQLAIYIIV 120
 QY 300 AGILCIYINWDCROHROEPRRTNGKCLVWGRAPSKIVASYTTSGETKSLTSGMWGL 359
 DB 121 AGILCIYINWDCROHROEPRRTNGKCLVWGRAPSKIVASYTTSGETKSLTSGMWGL 180
 QY 360 ARFHVYVPELISAFWTFVAFEDNLFAYFYVIFLTLLEFDRAKRDDRCRSRYKWKLY 419
 DB 181 ARFHVYVPELISAFWTFVAFEDNLFAYFYVIFLTLLEFDRAKRDDRCRSRYKWKLY 240
 QY 420 CEK 422
 DB 241 CEK 243

RESULT 7
 ID AAG23599 standard; Protein; 231 AA.
 AC AAG23599;
 XX
 DT 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 26966.
 DE Protein identification; signal transduction pathway; metabolic pathway;
 XX

KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KM termination sequence.
 XX
 OS Arabidopsis thaliana.
 PN EPI033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121925.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
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 PR 06-APR-1999; 99US-0128234.
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 PR 16-APR-1999; 99US-0129845.
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 PR 30-APR-1999; 99US-0132048.
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 PR 06-MAY-1999; 99US-0132486.
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 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
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PR	25-OCT-1999	9905-0161406
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PR	26-OCT-1999	9905-0161360
PR	26-OCT-1999	9905-0161361
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PR	29-OCT-1999	9905-0162143

Query Match	47.0%;	Score 1220;	DB 21;	Length 231;
Best Local Similarity	99.5%;	Pred. No. 2.2e-113;		
Matches 220;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;

QY	202	MSNAVLAVTYCIKOYEINCKSVSSMLVNTILMVYTKFPMWAGYWNMTDAHDGSGF	261
QY	202	MSNAVLAVTYCIKOYEINCKSVSSMLVNTILMVYTKFPMWAGYWNMTDAHDGSGF	261
Db	1	MSNAVLAVTYCIKOYEINCKSVSSMLVNTILMVYTKFPMWAGYWNMTDAHDGSGF	60
QY	262	YICMGCLVWVPYSVTSPGMLVNHPELQOLAYIIVAGILCIYINYDCCRQROEFRR	321
Db	61	YICMGCLVWVPYSVTSPGMLVNHPELQOLAYIIVAGILCIYINYDCCRQROEFRR	120
QY	322	NGKCLVWGRAPSKIVASITTTSGETKTSLLITSGMWGLAHHFHVPEILSAFTWYPALP	381
Db	121	NGKCLVWGRAPSKIVASITTTSGETKTSLLITSGMWGLAHHFHVPEILSAFTWYPALP	180
QY	382	DNFLAFVYVFTLLLPDRAKRDDRRRSRSGYKWKLYCEK	422
Db	181	DNFLAFVYVFTLLLPDRAKRDDRRRSRSGYKWKLYCEK	221

RESULT 8
AAI29333
ID AAI29333 standard; Protein; 475 AA
XX
AC AAI29333;
XX


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QY 63 TLIAKTIICYGAFAILLQLLP-----GKREGEPISPAGNRPYKANGIAAYF 111
D 93 TRKAQOLTYTLWTFQVLYTSLPDCCHKFLPGYVGIOGAVTPAGVNNKQINGLOAML 152
QY 112 VTLATYTLGLMWF-----GIFNPAIVYDH-LGEIFSAALIFGSFICVLLYIKGHVAPSS 164
D 153 LT-----HLMFANAHLLSWFSPTIIFDWMIPLMCMANILG-YAVSTFAMWKGYFFPTSA 206
QY 165 -DSGSCGNLIIDFYGMELYPRIKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKY 223
D 207 RDCKFTGNFNYMGMIEFNPRICKWDFKLFNGRPGIVAMTILINISFAKORELHSHV 266
QY 224 SDSMLVNTILMLVYTKFFWMEAGYWNMTDIAHNRGGEYICWGLVWVPSYTSFGVLY 283
D 267 TNAMVLVNLQAIYVIDEFWNETWYLTIDICDHFGWYLGWDCVWLPYLYTLOGLIYL 326
QY 284 NHPVELGTOLAIYIIVAGIICITINYDCDRQROEFRTNKGCLVWGRAPSKIVASYTTS 343
D 327 YHPVQLSTPHAVGVLLGLVGYIFRVANHOKDLFRRTDRCCLIMGRPKVIECSYTSAD 386
QY 344 GETKTSLLTSGMWGLARHFHYVEILSAFWWTVPALDFNFLAYFYVIFLTLIPDRAK 403
D 387 GQRHSHKLLIVSGFWGVARHNENYVDLMSIAYCLACGGHLLPFYITIMAILLTHRCR 446
QY 404 DDDRCRSKYGKWKLY 419
D 447 DEHRCAASKYGRDMERY 462

RESULT 10
AAM93573
ID AAM93573 standard; Protein; 475 AA.
AC AAM93573;
XX
XX 17-JUN-1999 (first entry)
DE Human Delta7-sterol reductase protein.
XX
XX Human; Delta7-sterol reductase; hereditary; Smith-Iemli-Opitz syndrome;
KM diagnosis; screening; double bond removal; 7-dehydrocholesterol;
KM organic polymeric ring; cholesterol.
XX
OS Homo sapiens.
XX
XX DE19739940-A1.
XX
XX 18-MAR-1999.
XX
XX 11-SEP-1997; 97DE-1039940.
XX
XX 11-SEP-1997; 97DE-1039940.
XX
XX 11-SEP-1997; 97DE-1039940.
XX
XX (GLOS/) GLOSSMANN H.
XX
XX Fitzky B, Glossmann H, Moebius F;
XX
XX WPI; 1999-191430/17.
XX
XX N-PSDB; AAX23387.
XX
XX Human Delta7-sterol reductase polypeptide - useful for diagnosis or
PT treatment of genetic defects e.g. hereditary Smith-Iemli-Opitz
PT syndrome
XX
XX Disclosure; Page 29-30; 62pp; German.
XX
XX This invention describes a human Delta7-sterol reductase. The encoding
CC DNA can be used to diagnose or correct human Delta7-sterol reductase gene
CC defects e.g. hereditary Smith-Iemli-Opitz syndrome, and to produce the
CC recombinant Delta7-sterol reductase polypeptide, which can be used to
CC replace a defective Delta7-sterol reductase enzyme in humans or other
CC animals. It is also useful to screen for Delta7-sterol reductase
CC inhibitors or to introduce and remove double bonds in synthetic and

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CC naturally occurring organic polymeric ring systems (Delta 7-sterol
CC reductase catalyses the conversion of 7-dehydrocholesterol to
CC cholesterol).
XX
XX Sequence 475 AA:
QY 13 ASMLSLAFCPPFVILLMTWVHOD-----GSYQTFGFFWENGVOGLINIM---FRP 62
D 41 ASYIFELIAP---FVYVFIMACDQYSCALGPVVDY-----TGHARLSDIMAKTPPI 92
QY 63 TLIAKTIICYGAFAILLQLLP-----GKREGEPISPAGNRPYKANGIAAYF 111
D 93 TRKAQOLTYTLWTFQVLYTSLPDCCHKFLPGYVGIOGAVTPAGVNNKQINGLOAML 152
QY 112 VTLATYTLGLMWF-----GIFNPAIVYDH-LGEIFSAALIFGSFICVLLYIKGHVAPSS 164
D 153 LT-----HLMFANAHLLSWFSPTIIFDWMIPLMCMANILG-YAVSTFAMWKGYFFPTSA 206
QY 165 -DSGSCGNLIIDFYGMELYPRIKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKY 223
D 207 RDCKFTGNFNYMGMIEFNPRICKWDFKLFNGRPGIVAMTILINISFAKORELHSHV 266
QY 224 SDSMLVNTILMLVYTKFFWMEAGYWNMTDIAHNRGGEYICWGLVWVPSYTSFGVLY 283
D 267 TNAMVLVNLQAIYVIDEFWNETWYLTIDICDHFGWYLGWDCVWLPYLYTLOGLIYL 326
QY 284 NHPVELGTOLAIYIIVAGIICITINYDCDRQROEFRTNKGCLVWGRAPSKIVASYTTS 343
D 327 YHPVQLSTPHAVGVLLGLVGYIFRVANHOKDLFRRTDRCCLIMGRPKVIECSYTSAD 386
QY 344 GETKTSLLTSGMWGLARHFHYVEILSAFWWTVPALDFNFLAYFYVIFLTLIPDRAK 403
D 387 GQRHSHKLLIVSGFWGVARHNENYVDLMSIAYCLACGGHLLPFYITIMAILLTHRCR 446
QY 404 DDDRCRSKYGKWKLY 419
D 447 DEHRCAASKYGRDMERY 462

RESULT 11
AAU39059
ID AAU39059 standard; Protein; 475 AA.
AC AAU39059;
XX
XX 16-JAN-2002 (first entry)
DE Human secreted protein pj323_2.
XX
XX Human; secreted protein; antiinflammatory; immunosuppressive;
KM nootropic; neuroprotective; antiarthritic; antimicrobial; vulnerary;
KM cytosolic; antidiabetic; vitruclide; antinfertility; anticonvulsant;
KM vasotropic; antiparkinsonian; immunostimulant; dermatological;
KM antitumoral; antitumor; antilicer; osteopathic; tranquilliser;
KM cerebroprotective; cytokine; cell proliferation; cell differentiation;
KM immune deficiency; severe combined immunodeficiency; SCID; tumour;
KM autoimmune disorder; multiple sclerosis; rheumatoid arthritis;
KM graft-versus-host disease; myeloid deficiency; wound healing; ulcer;
KM periodontal disease; osteoporosis; osteoarthritis; Alzheimer's disease;
KM Parkinson's disease; Huntington's disease; infection; cardiac disease;
KM stroke; sepsis; inflammatory bowel disease; contraceptive; immunogen;
KM food supplement; vaccine.
XX
XX Homo sapiens.
XX
XX WO200175068-A2.
XX
XX 11-OCT-2001.
XX

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PT New secreted proteins and encoding polynucleotides, useful in gene
PT therapies, particularly for preventing or treating autoimmune
PT disorders, cancer, graft-versus-host disease, wound, osteoporosis,
PT stroke or inflammations

XX Disclosure; Page 281-282; 349pp: English.

XX The invention relates to isolated polynucleotides (ABA90876-ABA90968 and
CC ABA90980) and encoded proteins (ABA55698-ABA55800), especially
CC polynucleotides SEQ ID NO 1 (ABA90876) and SEQ ID NO 19 (ABA90885) and
CC proteins SEQ ID NO 2 (ABA55698) and SEQ ID NO 20 (ABA55707) contained in
CC clones b3306-7 and yb8-1 respectively and the clones b3306-7 and yb8-1
CC are deposited with the American Type Culture Collection (ATCC) with
CC accession number 98599. The polynucleotides and encoded polypeptides have
CC cytosolic, anti-inflammatory, immunomodulator, vulnerability,
CC neuroprotective, activin, inhibin, chemotactic, haemostatic, thrombolytic
CC and anti-inflammatory activity and acting as cytokine modulators,
CC hematopoiesis regulators, tissue growth modulators and/or cadherin
CC suppressors. The polypeptides and polynucleotides are useful in gene
CC therapies, particularly for preventing, treating or ameliorating any of
CC the following diseases: immune deficiency and disorders: e.g. bacterial
CC or fungal infections, autoimmune disorders, cancer, systemic lupus
CC erythematosus or graft-versus-host disease; myeloid or lymphoid cell
CC deficiencies; wound, burns, incisions and ulcers, osteoporosis or
CC osteoarthritis; central and peripheral nervous system diseases and
CC neuropathies, e.g. Alzheimer's, Parkinson's disease, Huntington's
CC disease, amyotrophic lateral sclerosis or Shy-Drager syndrome;
CC haemophilia, cardiac infarction or stroke; inflammations, shock, sepsis
CC or systemic inflammatory response syndrome, ischaemia-reperfusion
CC injury, endotoxin lethality, arthritis, inflammatory bowel disease or
CC Crohn's disease; or tumours or cancers, pemphigus vulgaris or pemphigus
CC foliaceus.

XX Sequence 475 AA:

Query Match 26.9%; Score 698.5; DB 23; Length 475;
Best Local Similarity 35.3%; Pred. No. 7.2e-61;
Matches 154; Conservative 87; Mismatches 152; Indels 43; Gaps 10;

QY 13 ASMSLAFPPPPVLLMTVMVHOD-----GSVOTCFEFTFENVOGLINTW---PPR 62
DB 41 ASYFLLFLP---FIYIYIMCDQYSCALTPVDIV---TGHARLSDWARTPTPI 92
QY 63 TLIAKKIIFCYGAFEAALLQLLP-----GKRVESGPISPAGNRPYKANGLAAYF 111
DB 93 TRKAQLYTLMTVEQVLLYSLDPFCHKELPGVVGIGOBGAVTPAGVKNYQINGLOANI 152
QY 112 VTATATYGLMWF-----GIFNPAIYVDH-LGEIFSAIIFGSIIFCVLLYIKGVAPSSS 164
DB 153 LT-----HILMFANAHLLSWFSPTIIFDMWIPILMCANILG-YAVSTFAMVKGYFPPTSA 206
QY 165 -DSGSGCNLIIDFYMGMEIYPRIGKSPDIKVFNCGRFMSMAVLAIVYCIQYELNGVY 223
DB 207 RDKCFGNFNYNYMKGIEFNRKGFKMFDRKLFNGRPGVIAWTLINLSRAKORELASHV 266
QY 224 SDSMLVNTILMIVYTKFEMWAGYNTMDIAHDSRGFYICWGLVWVSPYSPGMIVY 283
DB 267 TNAMVAVNVLQAIYVIDEFNENETWYIKTDIDCHDFRGWLVGMDCWMLYVTLQGLYIV 326
QY 284 NHPEVGLQAIYIIVAGIICITINDDCRQREFRTNGKCLVWGRAPSKIVASTTTS 343
DB 327 YHVPQLSTPAVAVLLGLVGLYIIFVANHOKDLFRRTRGRCILWGRKPRVIECSTYSD 386
QY 344 GETKTSLLTSGMWGLARHFFHYVPELISAFPMVPALEFNTAFVIVFLTLLEPRAR 403
DB 387 GQRHSHKLLVSGFWARHFNHYGDLMSGLATCLACGGHLPFYITITWAILTHRCIL 446
QY 404 DDDRCRSKYGTWKLY 419
DB 447 DEHRCAASKYGRDWERY 462
RESULT 13

AA040884
ID AA040884 standard; Protein; 154 AA.
XX
AC AA040884;
XX
DT 18-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 50788.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
PN EP1033405-A2.
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
XX PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
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PR 25-AUG-1999; 99US-0150566.
PR 25-AUG-1999; 99US-0150984.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152263.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

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Query Match

25.1%; Score 651.5; DB 21; Length 154;

Best Local Similarity 77.9%; Pred. No. 7.4e-57; Matches 120; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

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QY 15 MSLIAFCPPVILLYTMVHODGSVTOTGEFNEVCV-QGLNIWPRPLIAKIIIFCY 73
DB 1 MLALSLCPPEVILLYTMVHADGSVRYTEHLRDHGLVLEGIKAIWMPPLVAKRIIFG 60
QY 74 GAFETIIDLPLPGKRVESPTSPAGNRVYKANGLAAYFVLTATYGLWFGIFNPATYVD 133
DB 61 GLPEAVIQLPLPGKRFESPTSPAGNVYKANG-LQAYAVTLITLYGLWFGIFNPATYVD 120
QY 134 HUGETFSALIFGSEFICVILYIKGHVAPSSSDSG 167
DB 121 HUGETFSALVFGSEFICVILYIKGHVAPSSSDSG 154

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AAB60760	ID	AAB60760 standard; peptide; 280 AA.
XX	AC	AAB60760;
XX	DT	27-MAR-2001 (first entry)
DE	Gene	13 related peptide #2.
KX		
KW	Secreted protein; gene therapy; vaccine; cancer; leukemia;	
KW	autoimmune disease; allergy; inflammation; graft rejection;	
XX	hyperproliferation; cardiovascular; infection.	
OS	Homo sapiens.	
PN	MO200076531-A1.	
PD	21-DEC-2000.	
PF	01-JUN-2000; 2000MO-US15137.	
PR	11-JUN-1999; 99US-0138625.	
PA	(HUMA-) HUMAN GENOME SCI INC.	
PI	Rosen CA, Ruben SM, Komatsuolis GA;	
DR	WPI; 2001-071148/08.	
PT	Nucleic acids encoding 47 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -	
PS	Disclosure; Page 514-515; 525pp; English.	
XX		
CC	The present invention relates to 26 secreted human proteins. The	
CC	proteins may be used in the prevention, diagnosis and treatment of	
CC	diseases associated with inappropriate polypeptide expression.	
CC	For example, they may be used in gene therapy or in vaccines.	
CC	Typical of diseases which are potentially treatable are cancers	
CC	(including leukemia), autoimmune diseases, allergies, inflammation,	
CC	graft rejection, hyperproliferation, cardiovascular diseases	
CC	(particularly critical limb ischemia and coronary disease) and any	
CC	involving abnormal angiogenesis, neurodegeneration and/or	
CC	infectious diseases.	
SQ	Sequence	280 AA;
	Query Match	23.3%; Score 604.5; DB 22; Length 280;
	Best Local Similarity	41.5%; Pred. NO. 8.4e-52;
	Matches 110; Conservative	60; Mismatches 94; Indels 1; Gaps
OY	156 KGVAVPSS-DSGSCGNLIIDFYWMELYPRIKGSFIDIKVFTNCRFGMGMVAVLATYYCI	214
Dd	3 KGVEFPSTADCKFTGNFFNYNMGIERNPRIKWFDPKLFNFGRPIVAMTLINLSFAA	62
OY	215 KOYEINKSKVSDSMLVTITLMLVUYTKRFPMWEENGIVNTMDIANHDGEGYICWGCLVWPVS	274
Dd	63 KKEBELSHVNANVANLVLDALITYIDFWNEFTWLKTIDICHDFGYLTQMGCVMPLPYI	122
OY	275 YTPRGMLVNHPRELOTOLATILYAIGLICIYNDDOROREFRRTNGKGLVAGRPSK	334
Dd	123 YTGIOGLIYHNHQJLSTPHAVGVLLGLVGYYIRPVANHQQDLFRKRJDRCGLIMGRPKY	182
OY	335 IVASYTTTSGETKTSLLTSGMWGLAHFHVPETLSAFWTYVALDNLAFVYVIFLT	394
Dd	183 IECSYTSADGOBHNSKLTVSGFMVAGRHFNVVYDLMGSLAICLAGGGHLIPFYIIYMA	242
OY	395 LLLFDRAKKRDDRCRXYGKYWKLY	419
Dd	243 ILTHRCLEDRHCASKYGRDWERY	267

Fri Jan 17 19:40:53 2003

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Page 18

Search completed: January 14, 2003, 14:15:10
Job time : 43 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 14, 2003, 14:17:29 ; Search time 13 Seconds
(without alignments)
710.377 Million cell updates/sec

Title: US-09-817-774-31
Perfect score: 2594
Sequence: 1 MAETVHSPIVTYASMLSLA.....RAKTKMQDAIDILLICML 476

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues
Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA.*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2594	100.0	476	10	US-09-817-774-31
2	2318	89.4	432	10	US-09-817-774-29
3	2313	89.2	432	10	US-09-817-774-39
4	2312	89.1	432	10	US-09-817-774-43
5	2247	86.6	411	10	US-09-817-774-45
6	2233	86.1	408	10	US-09-817-774-41
7	2182	84.1	399	10	US-09-817-774-37
8	1606	61.9	298	10	US-09-817-774-33
9	1606	61.9	323	10	US-09-817-774-35
10	710.5	27.4	471	10	US-09-817-774-27
11	698.5	26.9	473	10	US-09-729-674-12
12	698.5	26.9	475	10	US-09-817-774-26
13	553.5	21.3	427	10	US-09-817-774-23
14	540	20.8	426	10	US-09-817-774-22
15	500.5	19.3	424	10	US-09-817-774-25
16	97	3.7	615	9	US-09-738-626-6967
17	95.5	3.7	541	9	US-10-028-072-14
18	95.5	3.7	555	10	US-09-925-297-827
19	95.5	3.7	733	12	US-10-036-328A-4

20	95.5	3.7	1210	12	US-10-036-328A-2	Sequence 2, Appl1
21	94.5	3.6	500	12	US-10-033-109-4	Sequence 4, Appl1
22	94.5	3.6	541	10	US-09-809-545A-33	Sequence 33, Appl1
23	93	3.6	427	10	US-09-922-501-2	Sequence 2, Appl1
24	91.5	3.5	444	10	US-09-853-386-132	Sequence 132, Appl1
25	91.5	3.5	444	10	US-09-853-386-136	Sequence 136, Appl1
26	91.5	3.5	444	10	US-09-191-724-15	Sequence 15, Appl1
27	91.5	3.5	618	10	US-09-995-007-2	Sequence 2, Appl1
28	89.5	3.5	440	9	US-09-738-626-4646	Sequence 4646, Ap
29	89	3.4	420	10	US-09-853-386-129	Sequence 129, Ap
30	89	3.4	427	10	US-09-922-501-6	Sequence 6, Appl1
31	88	3.4	448	12	US-10-029-756-5	Sequence 5, Appl1
32	87.5	3.4	494	12	US-10-033-109-6	Sequence 6, Appl1
33	87.5	3.4	662	12	US-10-036-328A-8	Sequence 8, Appl1
34	87.5	3.4	714	10	US-09-818-264-2	Sequence 2, Appl1
35	87.5	3.4	1138	12	US-10-036-328A-6	Sequence 6, Appl1
36	87	3.4	259	10	US-09-905-176-20	Sequence 20, Appl1
37	86	3.3	526	9	US-09-738-626-5712	Sequence 5712, Ap
38	85.5	3.3	501	8	US-08-635-967-2	Sequence 2, Appl1
39	85.5	3.3	539	10	US-09-815-242-5139	Sequence 5139, Ap
40	85	3.3	446	9	US-10-136-517-19	Sequence 19, Appl1
41	84	3.2	390	10	US-09-925-302-661	Sequence 661, Ap
42	83.5	3.2	519	10	US-09-825-012-80	Sequence 80, Appl1
43	83	3.2	245	9	US-09-895-913A-48	Sequence 48, Appl1
44	83	3.2	321	10	US-09-886-055-123	Sequence 123, App
45	83	3.2	415	10	US-09-853-386-128	Sequence 128, App

ALIGNMENTS

RESULT 1	US-09-817-774-31	
Sequence 31, Application US/09817774		
Patent No. US2002012011A1		
GENERAL INFORMATION:		
APPLICANT: CHOE, Sunghwa		
APPLICANT: FELDMANN A., Kenneth		
TITLE OF INVENTION: DWFS MUTANTS		
FILE REFERENCE: 2225-0020 / 91020.002		
CURRENT APPLICATION NUMBER: US/09/817, 774		
PRIOR FILING DATE: 2001-03-26		
PRIOR APPLICATION NUMBER: 60/1792, 202		
NUMBER OF SEQ ID NOS: 45		
SOFTWARE: PatentIn Ver. 2.0		
SEQ ID NO 31		
LENGTH: 476		
TYPE: PRT		
ORGANISM: Arabidopsis thaliana		
US-09-817-774-31		
Query Match	100.0%; Score 2594; DB 10; Length 476;	
Best Local Similarity	100.0%; Pred. No. 4.8e-236;	
Matches 476; Conservative 0; Mismatches 0; Indels 0;		
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QY 1 MAETVHSPIVTYASMLSLAFCPPVILLMTVMHQDSVTQTGFEWENGVOGLINIMP 60		
DB 1 MAETVHSPIVTYASMLSLAFCPPVILLMTVMHQDSVTQTGFEWENGVOGLINIMP 60		
QY 61 RPTLAWKTIIFCYGAFEMILQLLPGRKREGEISFAGNRPYKANGLAAYVTATYIGL 120		
DB 61 RPTLAWKTIIFCYGAFEMILQLLPGRKREGEISFAGNRPYKANGLAAYVTATYIGL 120		
QY 121 WMFGIFNPAIVVDHGEIFSALEIFGFCVLLYTKGVAPASSSDSGCMLIIDFYWM 180		
DB 121 WMFGIFNPAIVVDHGEIFSALEIFGFCVLLYTKGVAPASSSDSGCMLIIDFYWM 180		
QY 181 ELYPRIGSFDIKVTNCRFGMSWAVLAVTYCIKQYEINGKVSQSMVLNVTILMLVYTK 240		
DB 181 ELYPRIGSFDIKVTNCRFGMSWAVLAVTYCIKQYEINGKVSQSMVLNVTILMLVYTK 240		
QY 241 FFWMEAGVWNTMDIADHDGFGFICWGLVWVPSTYTSQMTLVNHPVELGTQLAIIYILA 300		

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Db 241 FFWMEAGYWNMTMDIAHNRGFEYICWGLVWVPSVYTSFGMYLVNHPVELGTOLAIYILVA 300
QY 301 GILCIYINWDCDRQROEFRTNKGCLVWGRAPSKIVASTTTSGEFTSLTSLTSGMWGLA 360
Db 301 GILCIYINWDCDRQROEFRTNKGCLVWGRAPSKIVASTTTSGEFTSLTSLTSGMWGLA 360
QY 361 RHFHYVEILSAFFWTVPALFDNFLAYFYVIFLTLTLPRAKRDRCRSKYGYWKLVC 420
Db 361 RHFHYVEILSAFFWTVPALFDNFLAYFYVIFLTLTLPRAKRDRCRSKYGYWKLVC 420
QY 421 EKSNTGSFREFIDCNEVCSHFLITLITLRTLESSKDRAKTKQIDAIDLILICML 476
Db 421 EKSNTGSFREFIDCNEVCSHFLITLITLRTLESSKDRAKTKQIDAIDLILICML 476

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RESULT 2

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US-09-817-774-29
; Sequence 29, Application US/09817774
; Patent No. US2002012011A1
; GENERAL INFORMATION:
; APPLICANT: CHOE, Sungbwa
; APPLICANT: FELDMANN A., Kenneth
; TITLE OF INVENTION: Dwt5 MUTANTS
; FILE REFERENCE: 2225-0020 / 91020.002
; CURRENT APPLICATION NUMBER: US/09/817,774
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,202
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 432
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-09-817-774-29

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Query Match 89.4%; Score 2318; DB 10; Length 432;

Best Local Similarity 100.0%; Pred. No. 3.7e-210; Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 RPTLIAMKIIIFCYGAFEAIIQLLLPGKRVESGPISPAENRPPYKANGLAAYFVLATYGL 120
QY 121 WMEGIFNPAIYVDHIGEFISALIFGSFIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180
Db 121 WMEGIFNPAIYVDHIGEFISALIFGSFIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180
QY 181 ELIPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINRGSVDSMLVNTIIMLYVTK 240
Db 181 ELIPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINRGSVDSMLVNTIIMLYVTK 240
QY 241 FFWMEAGYWNMTMDIAHNRGFEYICWGLVWVPSVYTSFGMYLVNHPVELGTOLAIYILVA 300
Db 241 FFWMEAGYWNMTMDIAHNRGFEYICWGLVWVPSVYTSFGMYLVNHPVELGTOLAIYILVA 300
QY 301 GILCIYINWDCDRQROEFRTNKGCLVWGRAPSKIVASTTTSGEFTSLTSLTSGMWGLA 360
Db 301 GILCIYINWDCDRQROEFRTNKGCLVWGRAPSKIVASTTTSGEFTSLTSLTSGMWGLA 360
QY 361 RHFHYVEILSAFFWTVPALFDNFLAYFYVIFLTLTLPRAKRDRCRSKYGYWKLVC 420
Db 361 RHFHYVEILSAFFWTVPALFDNFLAYFYVIFLTLTLPRAKRDRCRSKYGYWKLVC 420
QY 421 EK 422
Db 421 EK 422

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RESULT 3

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US-09-817-774-39
; Sequence 39, Application US/09817774
; Patent No. US2002012011A1
; GENERAL INFORMATION:
; APPLICANT: CHOE, Sungbwa
; APPLICANT: FELDMANN A., Kenneth
; TITLE OF INVENTION: Dwt5 MUTANTS
; FILE REFERENCE: 2225-0020 / 91020.002
; CURRENT APPLICATION NUMBER: US/09/817,774
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,202
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 39
; LENGTH: 432
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-09-817-774-39

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Query Match 89.2%; Score 2313; DB 10; Length 432;

Best Local Similarity 99.8%; Pred. No. 1.1e-209; Matches 421; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAETVHSPIVTVASMLSLAFCEPPEVILLMTYVHODGSVTQTFGEFWENGVOGLINIMP 60
Db 1 MAETVHSPIVTVASMLSLAFCEPPEVILLMTYVHODGSVTQTFGEFWENGVOGLINIMP 60
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Db 61 RPTLIAMKIIIFCYGAFEAIIQLLLPGKRVESGPISPAENRPPYKANGLAAYFVLATYGL 120
QY 121 WMEGIFNPAIYVDHIGEFISALIFGSFIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180
Db 121 WMEGIFNPAIYVDHIGEFISALIFGSFIFCVLLYIKGHVAPSSSDSGSCGNLIIDFYWGM 180
QY 181 ELIPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINRGSVDSMLVNTIIMLYVTK 240
Db 181 ELIPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINRGSVDSMLVNTIIMLYVTK 240
QY 241 FFWMEAGYWNMTMDIAHNRGFEYICWGLVWVPSVYTSFGMYLVNHPVELGTOLAIYILVA 300
Db 241 FFWMEAGYWNMTMDIAHNRGFEYICWGLVWVPSVYTSFGMYLVNHPVELGTOLAIYILVA 300
QY 301 GILCIYINWDCDRQROEFRTNKGCLVWGRAPSKIVASTTTSGEFTSLTSLTSGMWGLA 360
Db 301 GILCIYINWDCDRQROEFRTNKGCLVWGRAPSKIVASTTTSGEFTSLTSLTSGMWGLA 360
QY 361 RHFHYVEILSAFFWTVPALFDNFLAYFYVIFLTLTLPRAKRDRCRSKYGYWKLVC 420
Db 361 RHFHYVEILSAFFWTVPALFDNFLAYFYVIFLTLTLPRAKRDRCRSKYGYWKLVC 420
QY 421 EK 422
Db 421 EK 422

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SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 45
 LENGTH: 432
 TYPE: PRF
 ORGANISM: Arabidopsis thaliana
 US-09-817-774-45

Query Match 89.1%; Score 2312; DB 10; Length 432;
 Best Local Similarity 99.8%; Pred. No. 1.3e-209;
 Matches 421; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAETVSPITVYASMLSLAFCEPPVILLMTYVHODGSVTOFGFEWENGVOGLINIMP 60
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 QY 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 DB 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
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 DB 181 ELYPRIGKSEDIKVTNCRFGMSMAVLAATYCIKQYEINGKVSMSLVNTILMLVYTK 240
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 DB 241 FFMWEAGYNTMDIAHDSGFEYICWGLVWPVSPTSFGMYLVNHPVELGTOLATYILA 300
 QY 301 GILCIYINDDCROQROEFRTNGKCLVWGRAPSKIYASVTTTSGEFTKSLTSGMWGLA 360
 DB 301 GILCIYINDDCROQROEFRTNGKCLVWGRAPSKIYASVTTTSGEFTKSLTSGMWGLA 360
 QY 361 RHRYVPELISAFETVPALFDFNLAIFYVIFLTLFDRAKDDDRCKSKYKWKLYC 420
 DB 361 RHRYVPELISAFETVPALFDFNLAIFYVIFLTLFDRAKDDDRCKSKYKWKLYC 420
 QY 421 EK 422
 DB 421 EK 422

RESULT 5
 US-09-817-774-43
 Sequence 43, Application US/09817774
 Patent No. US2002012011A1
 GENERAL INFORMATION:
 APPLICANT: CHOE, Sunghwa
 APPLICANT: FELDMANN A., Kenneth
 TITLE OF INVENTION: Dwf5 MUTANTS
 FILE REFERENCE: 2225-0020 / 91020.002
 CURRENT APPLICATION NUMBER: US/09/817,774
 CURRENT FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: 60/192,202
 PRIOR FILING DATE: 2000-03-27
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 43
 LENGTH: 411
 TYPE: PRF
 ORGANISM: Arabidopsis thaliana
 US-09-817-774-43

Query Match 86.6%; Score 2247; DB 10; Length 411;
 Best Local Similarity 100.0%; Pred. No. 1.6e-203;
 Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 RPTLIAMKIIIFCYGAFETAILQLLPKRVGEGPISPAKNRPYKANGLAAYVTLATYGL 120
 DB 61 RPTLIAMKIIIFCYGAFETAILQLLPKRVGEGPISPAKNRPYKANGLAAYVTLATYGL 120
 QY 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 DB 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 QY 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 DB 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
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 DB 181 ELYPRIGKSEDIKVTNCRFGMSMAVLAATYCIKQYEINGKVSMSLVNTILMLVYTK 240
 QY 241 FFMWEAGYNTMDIAHDSGFEYICWGLVWPVSPTSFGMYLVNHPVELGTOLATYILA 300
 DB 241 FFMWEAGYNTMDIAHDSGFEYICWGLVWPVSPTSFGMYLVNHPVELGTOLATYILA 300
 QY 301 GILCIYINDDCROQROEFRTNGKCLVWGRAPSKIYASVTTTSGEFTKSLTSGMWGLA 360
 DB 301 GILCIYINDDCROQROEFRTNGKCLVWGRAPSKIYASVTTTSGEFTKSLTSGMWGLA 360
 QY 361 RHRYVPELISAFETVPALFDFNLAIFYVIFLTLFDRAKDDDRCKSK 411
 DB 361 RHRYVPELISAFETVPALFDFNLAIFYVIFLTLFDRAKDDDRCKSK 411

RESULT 6
 US-09-817-774-41
 Sequence 41, Application US/09817774
 Patent No. US2002012011A1
 GENERAL INFORMATION:
 APPLICANT: CHOE, Sunghwa
 APPLICANT: FELDMANN A., Kenneth
 TITLE OF INVENTION: Dwf5 MUTANTS
 FILE REFERENCE: 2225-0020 / 91020.002
 CURRENT APPLICATION NUMBER: US/09/817,774
 CURRENT FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: 60/192,202
 PRIOR FILING DATE: 2000-03-27
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 41
 LENGTH: 408
 TYPE: PRF
 ORGANISM: Arabidopsis thaliana
 US-09-817-774-41

Query Match 86.1%; Score 2233; DB 10; Length 408;
 Best Local Similarity 100.0%; Pred. No. 3.3e-202;
 Matches 408; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAETVSPITVYASMLSLAFCEPPVILLMTYVHODGSVTOFGFEWENGVOGLINIMP 60
 DB 1 MAETVSPITVYASMLSLAFCEPPVILLMTYVHODGSVTOFGFEWENGVOGLINIMP 60
 QY 61 RPTLIAMKIIIFCYGAFETAILQLLPKRVGEGPISPAKNRPYKANGLAAYVTLATYGL 120
 DB 61 RPTLIAMKIIIFCYGAFETAILQLLPKRVGEGPISPAKNRPYKANGLAAYVTLATYGL 120
 QY 61 RPTLIAMKIIIFCYGAFETAILQLLPKRVGEGPISPAKNRPYKANGLAAYVTLATYGL 120
 DB 61 RPTLIAMKIIIFCYGAFETAILQLLPKRVGEGPISPAKNRPYKANGLAAYVTLATYGL 120
 QY 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 DB 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 QY 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 DB 121 WMEGIFNPAIVYDHLGEIFSALEFSCVLLYIKGHVAPSSDSCGMLIDIFYWGM 180
 QY 181 ELYPRIGKSEDIKVTNCRFGMSMAVLAATYCIKQYEINGKVSMSLVNTILMLVYTK 240
 DB 181 ELYPRIGKSEDIKVTNCRFGMSMAVLAATYCIKQYEINGKVSMSLVNTILMLVYTK 240
 QY 241 FFMWEAGYNTMDIAHDSGFEYICWGLVWPVSPTSFGMYLVNHPVELGTOLATYILA 300
 DB 241 FFMWEAGYNTMDIAHDSGFEYICWGLVWPVSPTSFGMYLVNHPVELGTOLATYILA 300
 QY 301 GILCIYINDDCROQROEFRTNGKCLVWGRAPSKIYASVTTTSGEFTKSLTSGMWGLA 360
 DB 301 GILCIYINDDCROQROEFRTNGKCLVWGRAPSKIYASVTTTSGEFTKSLTSGMWGLA 360

QY 361 RHHVYBELLSAFWTVPALFQNFVFLTLLEDRAKDDDC 408
 DB 361 RHHVYBELLSAFWTVPALFQNFVFLTLLEDRAKDDDC 408

RESULT 7

US-09-817-774-37
 ; Sequence 37, Application US/09817774
 ; Patent No. US2002012011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOE, Sunghwa
 ; APPLICANT: FELDMANN A., Kenneth
 ; TITLE OF INVENTION: DWF5 MUTANTS
 ; FILE REFERENCE: 2225-0020 / 91020.002
 ; CURRENT APPLICATION NUMBER: US/09/817,774
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/192,202
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 37
 ; LENGTH: 399
 ; TYPE: PRF
 ; ORGANISM: Arabidopsis thaliana
 US-09-817-774-37

Query Match 84.1%; Score 2182; DB 10; Length 399;
 Best Local Similarity 100.0%; Pred. No. 2e-197;
 Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAETVSPITVYASMSLAFCEPFFVILLMTVHODGSVTQTFGEFMEGVGLINIMP 60
 DB 1 MAETVSPITVYASMSLAFCEPFFVILLMTVHODGSVTQTFGEFMEGVGLINIMP 60
 QY 61 RPTLIAMKIIIFCYGAFEAIIQLLPGKRVESGIPSPAGNRPYKANGLAAYFVLATYGL 120
 DB 61 RPTLIAMKIIIFCYGAFEAIIQLLPGKRVESGIPSPAGNRPYKANGLAAYFVLATYGL 120
 QY 121 WMGFIENPAIYDHLGELIFSGFIICVLYIKGHVAPSSDSCGNLIIDFYWGM 180
 DB 121 WMGFIENPAIYDHLGELIFSGFIICVLYIKGHVAPSSDSCGNLIIDFYWGM 180
 QY 181 ELYPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKVS DSMVNTIIMLYVTK 240
 DB 181 ELYPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKVS DSMVNTIIMLYVTK 240
 QY 241 FFWMEAGYNTMTDIAHNRGFEYICWGLVWPVSYSYTPGMVLYNHPVELGTQAIYIIVA 300
 DB 241 FFWMEAGYNTMTDIAHNRGFEYICWGLVWPVSYSYTPGMVLYNHPVELGTQAIYIIVA 300
 QY 301 GILCIYINDDCRQROEPRFTRNKCLVWGRAPSKIVASTTTSGEKTSLTSGWGMGA 360
 DB 301 GILCIYINDDCRQROEPRFTRNKCLVWGRAPSKIVASTTTSGEKTSLTSGWGMGA 360
 QY 361 RHHVYBELLSAFWTVPALFQNFVFLTLLEDRAKDDDC 408
 DB 361 RHHVYBELLSAFWTVPALFQNFVFLTLLEDRAKDDDC 408

RESULT 8

US-09-817-774-33
 ; Sequence 33, Application US/09817774
 ; Patent No. US2002012011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOE, Sunghwa
 ; APPLICANT: FELDMANN A., Kenneth
 ; TITLE OF INVENTION: DWF5 MUTANTS
 ; FILE REFERENCE: 2225-0020 / 91020.002
 ; CURRENT APPLICATION NUMBER: US/09/817,774
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/192,202
 ; PRIOR FILING DATE: 2000-03-27

; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 33
 ; LENGTH: 298
 ; TYPE: PRF
 ; ORGANISM: Arabidopsis thaliana
 US-09-817-774-33

Query Match 61.9%; Score 1606; DB 10; Length 298;
 Best Local Similarity 100.0%; Pred. No. 1.9e-143;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAETVSPITVYASMSLAFCEPFFVILLMTVHODGSVTQTFGEFMEGVGLINIMP 60
 DB 1 MAETVSPITVYASMSLAFCEPFFVILLMTVHODGSVTQTFGEFMEGVGLINIMP 60
 QY 61 RPTLIAMKIIIFCYGAFEAIIQLLPGKRVESGIPSPAGNRPYKANGLAAYFVLATYGL 120
 DB 61 RPTLIAMKIIIFCYGAFEAIIQLLPGKRVESGIPSPAGNRPYKANGLAAYFVLATYGL 120
 QY 121 WMGFIENPAIYDHLGELIFSGFIICVLYIKGHVAPSSDSCGNLIIDFYWGM 180
 DB 121 WMGFIENPAIYDHLGELIFSGFIICVLYIKGHVAPSSDSCGNLIIDFYWGM 180
 QY 181 ELYPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKVS DSMVNTIIMLYVTK 240
 DB 181 ELYPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKVS DSMVNTIIMLYVTK 240
 QY 241 FFWMEAGYNTMTDIAHNRGFEYICWGLVWPVSYSYTPGMVLYNHPVELGTQ 292
 DB 241 FFWMEAGYNTMTDIAHNRGFEYICWGLVWPVSYSYTPGMVLYNHPVELGTQ 292

RESULT 9

US-09-817-774-35
 ; Sequence 35, Application US/09817774
 ; Patent No. US2002012011A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOE, Sunghwa
 ; APPLICANT: FELDMANN A., Kenneth
 ; TITLE OF INVENTION: DWF5 MUTANTS
 ; FILE REFERENCE: 2225-0020 / 91020.002
 ; CURRENT APPLICATION NUMBER: US/09/817,774
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/192,202
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: Patentln Ver. 2.0
 ; SEQ ID NO 35
 ; LENGTH: 323
 ; TYPE: PRF
 ; ORGANISM: Arabidopsis thaliana
 US-09-817-774-35

Query Match 61.9%; Score 1606; DB 10; Length 323;
 Best Local Similarity 100.0%; Pred. No. 2.1e-143;
 Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAETVSPITVYASMSLAFCEPFFVILLMTVHODGSVTQTFGEFMEGVGLINIMP 60
 DB 1 MAETVSPITVYASMSLAFCEPFFVILLMTVHODGSVTQTFGEFMEGVGLINIMP 60
 QY 61 RPTLIAMKIIIFCYGAFEAIIQLLPGKRVESGIPSPAGNRPYKANGLAAYFVLATYGL 120
 DB 61 RPTLIAMKIIIFCYGAFEAIIQLLPGKRVESGIPSPAGNRPYKANGLAAYFVLATYGL 120
 QY 121 WMGFIENPAIYDHLGELIFSGFIICVLYIKGHVAPSSDSCGNLIIDFYWGM 180
 DB 121 WMGFIENPAIYDHLGELIFSGFIICVLYIKGHVAPSSDSCGNLIIDFYWGM 180
 QY 181 ELYPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKVS DSMVNTIIMLYVTK 240
 DB 181 ELYPRIGKSPDIKFTNCRFGMSMAVLAATYCIKOYEINGKVS DSMVNTIIMLYVTK 240

QY 241 FFMWAGYMTMDIAHGRGFFYICWGLVWVPSYTSRGMVNHPELGTQ 292
 Db 241 FFMWAGYMTMDIAHGRGFFYICWGLVWVPSYTSRGMVNHPELGTQ 292

RESULT 10

US-09-817-774-27
 ; Sequence 27, Application US/09817774
 ; Patent No. US20020120111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOE, Sunghwa
 ; APPLICANT: FELDMANN A., Kenneth
 ; TITLE OF INVENTION: DWFS MUTANTS
 ; FILE REFERENCE: 2225-0020 / 91020.002
 ; CURRENT APPLICATION NUMBER: US/09/817,774
 ; PRIOR FILING DATE: 2001-03-26
 ; PRIOR APPLICATION NUMBER: 60/192,202
 ; PRIOR FILING DATE: 2000-03-27
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 27
 ; LENGTH: 471
 ; TYPE: PRF
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: S7R-RAT
 ; US-09-817-774-27

Query Match 27.4%; Score 710.5; DB 10; Length 471;
 Best Local Similarity 36.6%; Pred. No. 5e-59;
 Matches 157; Conservative 85; Mismatches 158; Indels 29; Gaps 9;

QY 13 ASMSLAFPCPFVILMTVMVHODSGVTQF--GFEMENVOGLINW---PRPTLIAMK 68
 Db 37 ASIFELLFAP--FIVYTFMACDQYSCSLAPALDIATGSHASLADIWAKTPPVTAKAQ 94
 QY 69 IIFCYGAFEAIIQLLP-----GKRVGPISPAQNPVYKANGLAAYFV----113
 Db 95 LYLAWVSFOYLKXSWLPDFCHRELPGVYGVGOGAITPRAGVYKKEVNGIOMLITHIIM 154
 QY 114 -LATYGLMFMFGJFNPAIVYDH-LGEIFSAIIFGSEFICVLLYIKGHVAPSS--DSGSGC 170
 Db 155 FVNAVYLLS---FSPYIIDNMIPILMCANILG-YAVSTFAMIKGYLFPSTAECKFTG 209
 QY 171 NLIDFWMGELPRIGKSPDIFVTNCRGMSMAVLAATYCIKOYEINGKYSDSMLN 230
 Db 210 NFEYNTVMGIEFNPRIKGFDEKLFENGPGIYAMTLINLSFAKOOELGHTVNSMILV 269
 QY 231 TIIMLVYVTKFFMWAGYMTMDIAHGRGFFYICWGLVWVPSYTSRGMVNHPELGTQ 290
 Db 270 NVLOAIYVLDFFWNMTWYLTIDICHDFGMYLGWGDVWLPLYTLGGLYLVYHNVOLS 329
 QY 291 TQAIYIVLIVGILCIYINVCDDROERFRRTNGKCLVWGRAPSKIYASTTSSGEFTKS 350
 Db 330 TPNALGILGLVGYIIFRNTNHQKDLFRRTDRCILGKPKPAICSYTSAGLGNHSHK 389
 QY 351 ILTSGMGLARHRYVPELISAFETVPALDFNLAIFYVYIFLLLEPRAKRDDRCS 410
 Db 390 LLYSGFMGVARHNPYTGDLMSGLAYCLACGGCHLLPYFIITWTILLTHRCRLDEHRCAN 449
 QY 411 KYGKYMKLY 419
 Db 450 KYGRDWEY 458

RESULT 11

US-09-729-674-142
 ; Sequence 142, Application US/09729674
 ; Patent No. US20010039335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jacobs, Kenneth
 ; APPLICANT: McCoy, John M.

APPLICANT: Lavalie, Edward R.
 APPLICANT: Collins-Racie, Lisa A.
 APPLICANT: Evans, Cheryl
 APPLICANT: Merberg, David
 APPLICANT: Treacy, Maurice
 APPLICANT: Agostino, Michael J.
 APPLICANT: Steinger II, Robert J.
 APPLICANT: Spaulding, Vikki
 APPLICANT: Wong, Gordon G.
 APPLICANT: Clark, Hilary
 APPLICANT: Fectel, Kim
 APPLICANT: Genetics Institute, Inc.
 TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
 FILE REFERENCE: 6055-64X
 CURRENT APPLICATION NUMBER: US/09/729,674
 PRIOR FILING DATE: 2000-12-04
 PRIOR APPLICATION NUMBER: 09/539,330
 PRIOR FILING DATE: 2000-03-30
 NUMBER OF SEQ ID NOS: 283
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 142
 LENGTH: 475
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-729-674-142

Query Match 26.9%; Score 698.5; DB 10; Length 475;
 Best Local Similarity 35.3%; Pred. No. 6.7e-58;
 Matches 154; Conservative 87; Mismatches 152; Indels 43; Gaps 10;

QY 13 ASMSLAFPCPFVILMTVMVHOD-----GSYTOFGFEMENVOGLINW---PRP 62
 Db 41 ASYIFELLFAP--FIVYTFMACDQYSCALTPVVDIV---TGARLSDIMAKTPPI 92
 QY 63 TLIAKRIIFCYGAFPAIIQLLP-----GKRVGPISPAQNPVYKANGLAAYF 111
 Db 93 TRKAQLYLVMTVFOYLYTSLPDCFKFLPGYVGIGOGAATPRAGVYKKEVNGIOML 152
 QY 112 VTLATYGLMFMFGJFNPAIVYDH-LGEIFSAIIFGSEFICVLLYIKGHVAPSS 164
 Db 153 LT-----HLIMFANAHLSWSPSTIIFDNIPLMCANILG-YAVSTFAMVKGFFPTSA 206
 QY 165 -DSGSGCNILIDFWMGELPRIGKSPDIFVTNCRGMSMAVLAATYCIKOYEINKY 223
 Db 207 ROCKFPGNFFYVMGIEFNPRIKGFDEKLFENGPGIYAMTLINLSFAKOOELGHTV 266
 QY 224 SDSMLVNTILMLVYVTKFFMWAGYMTMDIAHGRGFFYICWGLVWVPSYTSRGM 283
 Db 267 TNANVLVNVLOAIYVLDFFWNMTWYLTIDICHDFGMYLGWGDVWLPLYTLGGL 326
 QY 284 NHPVELGQOLAIYIVLIVGILCIYINVCDDROERFRRTNGKCLVWGRAPSKIY 343
 Db 327 YHPVOLSTPRHAGVLLGLVGYIIFRNVANHOKDLFRRTDRCILGKPKPAICSY 386
 QY 344 GFTKSLITSGMGLARHRYVPELISAFETVPALDFNLAIFYVYIFLLLEPRAKR 403
 Db 387 GORHNSKILLSGFMGVARHNPYTGDLMSGLAYCLACGGCHLLPYFIITWTILL 446
 QY 404 DDDRCRSKYGYMKLY 419
 Db 447 DEHRCASXYGRDWEY 462

RESULT 12

US-09-817-774-26
 ; Sequence 26, Application US/09817774
 ; Patent No. US20020120111A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHOE, Sunghwa
 ; APPLICANT: FELDMANN A., Kenneth
 ; TITLE OF INVENTION: DWFS MUTANTS
 ; FILE REFERENCE: 2225-0020 / 91020.002
 ; CURRENT APPLICATION NUMBER: US/09/817,774

CURRENT FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: 60/192,202
 PRIOR FILING DATE: 2000-03-27
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 26
 LENGTH: 475
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: STR-HUMAN
 US-09-817-774-26

Query Match 26.9%; Score 698.5; DB 10; Length 475;
 Best Local Similarity 35.3%; Pred. No. 6,7e-58;
 Matches 154; Conservative 87; Mismatches 152; Indels 43; Gaps 10;

13 ASMLSLAFCPPEVILLMTWVHOD-----GSVTFQTFEFGWENGVOGLINIV---PRP 62
 41 ASYIFLLLPAP---FIVYFIMACDQYSCALTPVVDIV---TGHARLSIDIMAKTPPI 92
 63 TLIAKIIIFCYGAFEAIIQLLP-----GKRVGPISPAGNRPYKANGLAAYF 111
 93 TRKAAQLYTLWTFQVLLTSLPDCHEKFLPGYVGIGQGAATPAGVYVKKQIINGLQAML 152
 112 VTLATYGLMWF-----GIFPAIYVDH-LGEIFSALIFGSEFICVLLYIKGHVAPSSS 164
 153 LT-----HLMTFANAHLSWFSPTIIFEDWIPILMCANILG-YAISTFAMVGVFFPISA 206
 165 -DSGSGNLIIDFYWGMELYPRIKSEPIKVTNCRFGMSNAVLAVTYCIKQYINCKV 223
 207 RCKKFTGNFNYMMGIEFNPRIGKWFDEKLFENGPRGIVAWTLINLSFAAKORELHSHV 266
 224 SOSMLVNTLIMLVYVTKFEFMEAGYWNMTMDIAHDSGEYICGCLVWSPVYTSQMYLY 283
 267 TNAWLVNVLQAIYVDFEWMETWYTKTIDICHDFGWLIGWDCWMLPYLTLOGLIY 326
 284 NHEVELGTOLAIYILVAGIYINYDCROKROEFRTNGKCLVWGRAPSKIVASYTTTS 343
 327 YHVQVSTPHAVGVLLGLGVYIFRVAHQDLFRRTDGRCLIMGRKRVIECSVTSAD 386
 344 GEFKTSLLTSGWGLARHFFHYPELLSAFMTVPALFENFLATYVFLTLTLLDRACK 403
 387 GQRHSHKLLVSGFWYARHFNVDLMSIACLAGGSHLLPYIITMALLTHRCIL 446
 404 DDDRCRSKYGKWKLY 419
 447 DEHRCAKSKTGRDWERY 462
 Db

RESULT 13
 US-09-817-774-23
 Sequence 23, Application US/09817774
 Patent No. US2002012011A1

GENERAL INFORMATION:
 APPLICANT: CHOE, SungHwa
 APPLICANT: FELDMANN A., Kenneth
 TITLE OF INVENTION: DWFS MUTANTS
 FILE REFERENCE: 2225-0020 / 91020.002
 CURRENT APPLICATION NUMBER: US/09/817,774
 CURRENT FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: 60/192,202
 PRIOR FILING DATE: 2000-03-27
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 23
 LENGTH: 427
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: LBR-RAT
 US-09-817-774-23

Query Match 21.3%; Score 553.5; DB 10; Length 427;
 Best Local Similarity 33.0%; Pred. No. 2.5e-44;
 Matches 138; Conservative 65; Mismatches 176; Indels 39; Gaps 11;

16 LSLIAFCPPVILLMTWVHODGSVYQ-----TFQEFWENGVOGLINIMPRTLAMKI 69
 28 LTIMLGPACVFLLLQCAQKDFLQFPPELPALRELMARVGVYLLM----- 77
 70 IFYGAFAEAIQLLLPKRVGPISPAGNRPYKANGLAAYFVTLATYGLMWFIFNPA 129
 78 FE-----LQALFSLIPYKRYVEGTPVNDGRRLKRLNGLVAFILTSAA-VGTAFWMIELY 132
 130 IYVDHGEIFSALIFGSEFICVLLYIKGHVAPSSSDS-GSGCNLIIDFYWGMELYPRIK 188
 133 YLYTHFLOFMAAIVFVSVLVYLAARSLKVPREDLSPASSNAVVDFFIGRELNPRIG- 191
 189 SFDIKVTNCRFGMSNAVLAVTYCIKQYINCKVSDSM---LVNITIMLVYVTKFEFWE 245
 192 AFDKFECELRPGILGVVNVNLVNLAEKRVQERSAPSLMTLVNS-POLLVYVDALMFE 250
 246 AGYWNMTMDIAHDSGEYICGCLVWSPVYTSQMYLVNHPVELGTOLAIYILVAGIIC 305
 251 EALLTMDIHDGFMALAFGLDVTWVFTYSIQAFIYVNHQPOLSMPLT-SVITALKLG 309
 306 YINYDC-DROKROEFRTNGKCLVWGRAPSKIVASYTTTSGEFTSLLISGWMGLARH 364
 310 YVIFRCANSQKNAPRKN-----PTDKLAHLKTIPTSTKSLVSGWGFVYRHPN 359
 365 YVPEILSAFMTVPALPDNFAVYVFLTLTLLDRACKRDDDCRSKYGKWKLYCEK 422
 360 YLGLIMALASLPCGHNHLLPYVYLYFTALLIHRARDEHOCRRKRYGLAMWKYCOR 417
 Db

RESULT 14
 US-09-817-774-22
 Sequence 22, Application US/09817774
 Patent No. US2002012011A1
 GENERAL INFORMATION:
 APPLICANT: CHOE, SungHwa
 APPLICANT: FELDMANN A., Kenneth
 TITLE OF INVENTION: DWFS MUTANTS
 FILE REFERENCE: 2225-0020 / 91020.002
 CURRENT APPLICATION NUMBER: US/09/817,774
 CURRENT FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: 60/192,202
 PRIOR FILING DATE: 2000-03-27
 NUMBER OF SEQ ID NOS: 45
 SOFTWARE: Patent Ver. 2.0
 SEQ ID NO 22
 LENGTH: 426
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: LBR-HUMAN
 US-09-817-774-22

Query Match 20.8%; Score 540; DB 10; Length 426;
 Best Local Similarity 32.7%; Pred. No. 4.6e-43;
 Matches 142; Conservative 65; Mismatches 157; Indels 70; Gaps 16;

8 PIVYIASML-----SLIACPPPEVIL--LMTWVHODGSVYTFQEFWENGVOGLINI 58
 34 PVFLFLMLCMKOKDPDLSNPPLPALYELMETRY-----FQVY----- 73
 59 WPRPTLIMWKIIFCYGAFEAIIQLLP-GKRVGPISPAGNRPYKANGLAAYFVTLATY 117
 74 -----LIMFLI-----QVLFILPPIGKYVEGTPVNDGRRLKRLNGLVAFILTSAAV- 119
 118 LGLMWFIFNPAIYVDHGEIFSALIFGSEFICVL---LYIKGHVAPSSSDS-GSGCNL 172
 120 IGTSLFGQVEFHYVYSH---FLOFALAAVFCVLLSVYIMRSIKAPRNDLSPASSGNA 175
 173 IIDFYWGMELYPRIKSEPIKVTNCRFGMSNAVLAVTYCIKQYINCKVSDSM---LV 229
 Db

Db 176 YDFEIGRELNPRIIG-TEFLKXFCGLRPLIGWVIVINLMMLAEKIDDRRAVPSLIMLV 234
QY 230 NTILMLVVTKEFWMEAGYMTMDIAHNRGGEYICMGVLVWPVSYSRPGYLVNHPREL 289
Db 235 NS-FOLLVVDALMNEELLTMTDIIHDFGFMALFGDLVWPVPLYSQAYLSHPMEV 293
QY 290 GTQALVILVAGILCIYIN-DCDROROEFRRTNGKCLWMCRAPSKIVASYTTSGETKT 348
Db 294 SMPMASLIIVLK-LCGYVIFRGANSQKNAFRKN-----PSDKLAHLKTIHTSSG 342
QY 349 SLLTSGMWGLARHGHVPELLSAFMTVPALFDNFAYFVIFLTLFEDRARDDRC 408
Db 343 KNLVSGMWGFRHPNPLGDLIMALMSLPCGFNHLIPYFYIYFTMLVHREARDEYHC 402
QY 409 RSKYGYKWLKCEK 422
Db 403 KKTGVAMEKYCOR 416

RESULT 15
US-09-817-774-25
; Sequence 25 Application US/09817774
; Patent No. US2002012011A1
; GENERAL INFORMATION:
; APPLICANT: CHOE, Sunghwa
; APPLICANT: FELDMANN A., Kenneth
; TITLE OF INVENTION: DWIS MUTANTS
; FILE REFERENCE: 2225-0020 / 91020.002
; CURRENT APPLICATION NUMBER: US/09/817,774
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,202
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 25
; LENGTH: 424
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SLAR-YEAST
US-09-817-774-25

Query Match 19.3%; Score 500.5; DB 10; Length 424;
Best Local Similarity 32.5%; Pred. No. 2,4e-39;
Matches 128; Conservative 67; Mismatches 172; Indels 27; Gaps 11;

QY 43 TFGFFWENGVOG-----LINMPRLPLIAWKILFCYGAFEALLOLL--LPGRVREG- 91
Db 32 SFGSFYICNBERGCPAKFSKISHIKPTPLFDQKSLIYLMLFSPULLMKCTNGKMAKGT 91
QY 92 PISFAGNRPVYKANGL-AAFVTLATYLGMLWGFENPAIYDH-LGEIFSALIFGSFIF 149
Db 92 PIDKGRTRLKLKINGENSACLILGVCTSIYLLGASCMERIMDNFIQLMFAAYVF-SVL 150
QY 150 CVLLYINGHVA PSS-SDSGSGNLIIDPYWMELYPRIKSFIDIKVFTNCRFGMSWAVL 208
Db 151 CTFCYVOSFEGKQOLAKGTSIGNILFDFGRSLNPRIG-NFDIKCFCLRPGLIMVVF 209
QY 209 AVTYCICQY-EINGKVSDSLVTILMLVYVTFEWMAGYMTMDIAHNRGGEYICWGC 267
Db 210 DIAFACHQYLVLAGRITDSMLVLIIFHTWYVLDLINESAVLITMDITTDGFGYMLSGD 269
QY 268 LWWPVSYYTSPGMYLVNHPVELGTQALVILVAGIICITINYDODROROEFRRTNGKCLV 327
Db 270 LWWPFLYSLQARYLAHPVDLGLVKTALILCLOFLGYIFRGANGCKNFRSPND-- 326
QY 328 WGRAPSKIVASYTTSGETYTSLLTSGMWGLARHGHVPELLSAFMTVPALFDNFPLAY 387
Db 327 ---PKLHLKFIOTKRGTK---LITSGWGMMAHINYPGDWIMAMACLPAGFGSPIFY 379
QY 388 FYVIFLTLLEFDRAKRDDRCRSKYGYWKLYCE 421

Db 380 FYVAYFGVLLVHNRARDHRCRVKYGEDMEKYCK 413

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